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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                Title:
Perfect score:
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235
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Gapop 10.0 ,
                                                                                                                                                                               219241 seqs, 76174552 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

A;Molecule type: DNA A;ResLidues: 1-353 <RES> A;Cross-references: GB:L04788; NID:g144023; PIDN:AAA22963.1; PID:g144024 C;Genetics:

A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Gene: vmp17

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

SUMMARIES

) i	Se	27	26	25	24 /	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	N	1		Result
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RESULT 1 140300 outer membrane lipoprotein - Borrelia herms C;Species: Borrelia hermsii C;Date: 12-Aug-1996 #sequence_revision 12-Au C;Accession: 140300 R;Restrepo, B.I.; Kitten, T.; Carter, C.J.; Mol. Microbiol. 6, 3299-3311, 1992 A;Title: Subtelomeric expression regions of A;Reference number: 140300; MUID:93133110 A;Accession: 140300 A;Status: oreliminary: translated from GB/E		45 5	44 5						38 50.5								30 5	
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lipoprotein - Borre elia hermsii 1996 #sequence_revi 0300 6, 3299-3311, 792 0meric expression r beer: I40300; MUID:9 0300		1.3	1. 3	1.3	1.ω	1.3	1.3		21.5		. 5	5	1.7	21.7	21.7	21.7	21.7	
in - 1 sii sii [uence [uence] [uence] [uence] [uence] [uence]		648	630	412	362	338	247	77	1229	1219	694	284	649	556	391	388	388	
Borr rev Car 199		Ν	Ν	N	N	2	Ν	2	ν,	N	2	2	ಬ	N	2	2	₩.	
ii ug-1996 # Infante, Borrelia	ALIGNMENTS	A48646	C84453	B81176	S73454	T36785	T48878	F69219	A56068	161713	T30725	\$66520	T04005	F82342	T36311	H85573	SYECSB	
text_change 08-Oct-1999 D.; Barbour, A.G. hermsii linear plasmids are high		amine oxidase (cop	probable selenium.	hypothetical prote	probable GTP-bindi	hypothetical prote	proteasome psmA, a	conserved hypothet	co-repressor prote	co-repressor prote	probable abortive	tropomyosin, fast		methyl-accepting c	probable lipase -	succinyl-CoA synth	succinateCoA lig	

Query Match 26.8%; Score 63; DB 2; Length 246; Best Local Similarity 39.0%; Pred. No. 1.7; Matches 16; Conservative 6; Mismatches 19; Indels 0; Gaps 0;	A; Nolecule type: DNA A; Residues: 1-246 <bar> A; Residues: 1-246 <bar> A; Cross-references: GB: 211876 C; Comment: This spirochete eludes the immune system to cause the disease relapsing fe C; Keywords: membrane protein</bar></bar>	R;Barbour, A.G.; Carter, C.J.; Burman, N.; Freitag, C.S.; Garon, C.F.; Bergstroem, S. Infect. Immun. 59, 390-397, 1991 A;Title: Tandem insertion sequence-like elements define the expression site for varia A;Reference number: A43579; MUID:91099991	RESULT 2 A43579 A43579 Vmp7 protein homolog - Borrelia hermsii C;Species: Borrelia hermsii C;Species: Pa-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Mar-1993 C.Accession: A43579	Qy 3 TNPIDAAIGGSADRNAEAFDKMKKDDQIAAAMVLRGMAKDGQFAL 47 - : - : - - - - - - - - - - - - -	Query Match 34.9%; Score 82; DB 2; Length 353; Best Local Similarity 40.0%; Pred. No. 0.01; Matches 18; Conservative 8; Mismatches 19; Indels 0; Gaps 0;
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C: Keywords: GTP; GTP binding F;8-15/Region: nucleotide-b; F;70-74/Region: GTP binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mycoplasma genitalium
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 02-Feb-2001
C;Accession: F64202: T09682
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.I.
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Rccession: F64202
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:U39680; GB:L43967; NID:g1045681; PID:g1045693; TIGR:MG024
A;Experimental source: strain G-37
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, M.; Fuhrmann, J.L.; Nguyen, D.T.; Utterback, T.; Saudek, D.M.; Phillips, C.A.; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable GTP-binding protein - Mycoplasma genitalium C;Species: Mycoplasma capit==11...
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                                                                                                                                                                                                                A; Gene: MG024
                                                                                                                                                                                                                                      C; Genetics:
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A; Residues: 1-367 <FRA>
                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, October 1998 A;Reference number: Z16818 A;Recession: T09682 A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Accession: F83570
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, I. Lory, S.; Olson, M.V.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U39681; NID:g3844626; PID:g3844633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-353 <5TO>
A; Residues: 1-353 <5TO>
Coss-references: GB:AE004496; GB:AE004091; NID:g9946468; PIDN:AAG03988.1; GSPDB:GN001
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                                                                                                          ;Superfamily: yeast probable purine nucleotide-binding protein YBR025c; Keywords: GTP; GTP binding; nucleotide binding; P-loop; 8-15/Region: nucleotide-binding motif A (P-loop)
Query Match
Best Local Similarity
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idues: 1-367 <TIGR>
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12; Conserv
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42.9%;
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K.R.; Kas,
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A.; Larbig,
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                       12
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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 02-Mar-2001 **sequence_revision 02-Mar-2001 **text_change 31-Mar-2001 C; Accession: H86191 R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Map position: 4
A:Introns: 43/1; 156/3; 497/3; 543/3
C:Superfamily: gamma-glutamyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma-glutamyltransferase homolog T17Al3.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 18-Feb-2000
C;Accession: T13432
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AL096692; GSPDB:GN00062; ATSP:T17A13.30 A;Experimental source: cultivar Columbia; BAC clone F17A13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: Z17683
A; Accession: T13432
                                                                                                                                                                A;Cross-references: GB:AE005172; NID:g6850304; PIDN:AAF29381.1;
                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-500 <STO>
                                                                                                                                                                                                                                  A; Status: preliminary
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A; Residues: 1-637 <BEV>
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                        Local
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                     24.7%;
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                     Score 58; DB
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 58.5;
Pred. No. 16;
Mismatche:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
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                                         Length 500;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O.; Alon
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                                                                                                                                                                                                                                                                                                                                                                                                      Marzie
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GSADRNAEAFDKMKKDDQIAAAMVLRGMAKDG

43

Conservative

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C; Accession: D86269

R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID: 21016719

A; Accession: D86269
C;Accession: S59069
R;Schulz, T.C.; Hopwood, B.; Rathjen, P.D.; Wells, Biochem. J. 311, 219-224, 1995
A;Title: An unusual arrangement of 13 zinc fingers
                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change
                                                                                                                                            S59069
Z13 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Burman, N.; Bergstroem,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: S11981
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C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999
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A; Residues: 1-364 <BUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lecule type: DNA
idues: 1-797 <STO>
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                                                                                                                                                                                                                                                                                                        12 GSADRNAEAFDKMKKD----DQIAAAMVLRGMAKDGQF 45
                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                           GRIDEALSLFNQMKADGLSPDLVAYSIVIHGLCKLGKF
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                                                                                                                                                                                                                                                                                                                                                                               Score 56; DB Pred. No. 42;
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  fingers in the vertebrate
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                                                 J.R.E.
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  gene
  Z13
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A;Gene: sdhA C;Superfamily: fumarate

reductase flavoprotein; 3-oxosteroid 1-dehydrogenase homology

A; Experimental C; Genetics: A; Cross-references: A; Molecule type: DNA A; Residues: 1-611 <MAT>

source:

EMBL:Y07709; PIDN:CAA68982.1 >e: strain SP1 /28

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A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis A;Reference number: A71400; MUID:98121113 A;Accession: F71401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.;.Goodman, H.; Dean, C.; Bergkamp, R.; P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, Nature 391, 485-488, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:U14556; NID:g608136
C;Superfamily: POZ domain homology
F;10-108/Domain: POZ domain homology <POZ>
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A;Accession: S59069
A;Status: preliminary
                                                             R;Mattar, S.; Souquet, M.; Henrich, H.J.; Engelhard, M. submitted to the EMBL Data Library, August 1996 A;Description: The first fully resolved primary structu
                                                                                                                                                                          succinate dehydrogenase chain A homolog N;Alternate names: flavoprotein homolog C;Species: Natronomonas pharaonis
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A;Status: preliminary; translated
                      A; Accession: T44962
                                           A; Reference number: 222881
                                                                                                                                 C; Accession: T44962
                                                                                                                                                        C; Date:
                                                                                                                                                                                                                                            T44962
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A; Residues: 1-258 <BEV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, ernoft, A.; Mores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998
C;Accession: F71401
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A; Residues: 1-794 < SCH>
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                  107
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                                                                                                                                                     21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Mar-2000
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                                                                                                                                                                                                                                                                                                                                  PLANTLVNVYGKCGAASHALQVFDEMPHRDHIAWASVLTAL 147
                                                                                                                                                                                                                                                                                                                                                                                                                      15; Conser
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18; Conser
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Pred. No.
      from
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Pred. No. 64;
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    GB/EMBL/DDBJ
                                                                                                                                                                                                                     [imported] - Natronomonas pharaonis
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23;
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Rechman, S.;
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QY
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A;Map position: 4
A;Introns: 20/1; 49/1; 78/1; 98/1; 793/2; 891/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein M70.3 - Caenorhabditis elegans C;Species: Caenorhabditis clegans C;Species: Caenorhabditis clegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T33030
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C; Superfamily: Arabidopsis thaliana hypothetical protein At2g41080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
Lle: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
Leference number: A85001; MUID:20083488
A;Accession: B85153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein AT4g14050 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 C;Accession: B85153
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-686 <STO>
                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-915 <MIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                          ler, N.; Wamsley, P.; Twyman, B.
tted to the EMBL Data Library, February 1998
cscription: The sequence of C. elegans cosmid M70
Reference number: Z21266
Accession: T33030
                                                                                                                                                                     Query Match
Best Local
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Best Local Similarity 36.6%;
Matches 15; Conservative
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                                                                     PSDEAITDLLNIGGVKLKDLETFDKTKVDDVIA 162
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                                                                                                                                                   15;
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Similarity 35.1%;
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Pred. No.
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Pred. No. 57;
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Pred. No. 64;
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86;
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                                                                                                                                                                                   Length 915;
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A; Molecule type: DNA
A; Residues: 1-941 <a href="https://doi.org/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Nelson, J.; Langston, Y.
submitted to the EMBL Data Library, December 1996
A; Description: The sequence of C. elegans cosmid 7
A; Reference number: Z20105
A; Accession: T25888
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A;Residues: 1-2098 <NEL>
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
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A;Map position: 4
A;Introns: 20/1; 40/1; 60/1; 80/1; 774/2; 892/3
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                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: myosin motor domain homology E;65-720/Domain: myosin motor domain homology <MMO>
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A; Introns: 6/3;
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A; Accession: T33032
                                                                                                                                                            Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                       21 FDKMKKDDQI-AAAMVLRGMAKDGQFA 46
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15; Conserv
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48.1%;
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Pred. No. 2
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88;
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Result
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Maximum Match 100%
Listing first 45 summaries
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PROBABLE GTP-BINDING PROTEIN MG024.
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SEQUENCE
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                                                                   Plasmid
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01-MAY-1991 (Rel. 18,
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STRAIN-SSP. HS1 SEROTYPE
               SEQUENCE FROM N.A
                                        NCBI_TaxID=140;
                                                        Bacteria;
                                                                                   Borrelia hermsii
                                                                                                 VMP21
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MEDLINE=96026346; PubMed=7569993;
Mraser C.M., Gocayne J.D., White O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                      Spirochaetales;
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41198 MW;
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Last annotation updat
                                                                                                                                                     Created)
                                                      Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                 Score 59; DB 1; Length 367; Pred. No. 3.6;
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GTP (POTENTIAL).
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RESULT 4

Z151_MOUSE STANDARD; PRT; 794 AA.

ID Z151_MOUSE STANDARD; PRT; 794 AA.

AC Q60831; Q60699;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation updute)
DE ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITI.

DE PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).
GN ZNF151 OR ZFP100.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vortebra
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muri
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RP SEQUENCE FROM N.A.
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Barstad P.A., Coligan J.E., Raum M.G., Barbour A.G.;
Barstadle major proteins of Borrelia hermsii. Epitope mapping
partial sequence analysis of CMBr peptid:s.";
J. Exp. Med. 161:1302-1314(1985).
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Mol. Microbiol. 6:3299-3311(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91171872; PubMed:1706456; Burman N., Bergstroem S., Restrepo B.I., Barbour A.G.; Burman N. Bergstroem S. Restrepo B.I., Barbour A.G.; The variable antigens Vmp7 and Vmp21 of the relapsing fever bacterium Borrelia hermsii are structurally analogous to the VSG proteins of the African trypanosome."; moi. Microbiol. 4:1715-1726(1990).
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PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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STRAIN-SSP. HS1 SEROTYPE
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InterPro; IPR000680; Borrelia_lipo.
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SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPI
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364 /
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Pred. No. 8.5;
10; Mismatches
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N-ACYL DIGLYCERIDE (PROBABLE), 16598B639HE63776 CRC64;
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                                                       Craniata; Vertebrata;
Sciurognathi; Muridae;
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SMART; SM00325; ZnF_C2H2; 13.
PROSITE; PS50097; BTB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 13.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 13.
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Pfam; PF00096; zf-C2H2; 13.
PRINTS; PR00048; ZINCFINGER.
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the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
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Schulz T.C., Hopwood B., Rathjen P.D., Wells J.R.E.;
"An unusual arrangement of 13 zinc fingers in the ve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXAMINED.
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. J. 311:219-224(1995).
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114
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SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .ear protein;
LAEP-SSTTGESADASAVEGGDKRAKDEKAAATMLSRLGQAR 154
                                            LTNPIDAAIGGSADRNA-EAFDKMKKDDQIAAAMVLR-GMAK 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration
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U14556; AAA85493.1;
P08047; 1SP2.
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18; Conserv
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TISSUE=Kidney;
                                                                                           Conservative
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                                                                                                                                                                                                                86664 MW;
                                                                                                                  23.2%;
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                                                                                      Score 54.5; [Pred. No. 30; 6; Mismatches
                                                                                                                                                                                                                                 C2H2-TYPE.
G -> A (IN
N -> K (IN
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-> K (IN REF. 2).
FFF88E56EDEBF7ED CRC64;
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                                                                                                                                      Length 794;
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P40564;
01-FEB-1995 (Rel. 3
01-FEB-1995 (Rel. 3
20-AUG-2001 (Rel. 4
HYPOTHETICAL 48.6 H
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"A new genetic locus in Sinorhizobium meliloti is involved stachydrine utilization.";
Appl. Environ. Microbiol. 64:3954-3960(1998).
-!- FUNCTION: POSSIBLE NADH-DEPENDENT OXIDASE, FUNCTIONS ASDEMETHYLASE THAT CONVERTS N-METHYLPROLINE TO PROLINE.
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000205; NAD_binding.
InterPro; IPR001155; Oxidored_FMN.
Pfam; PF00724; oxidored_FMN; I.
Oxidoreductase; NAD; FAD; Flavoprotein; Plasmid.
SEQUENCE 580 AA; 63938 MW; 40BDA5DC5F096F3D
STRAIN=S288C / AB972;
Barrell B.G., Badcock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE N-METHYLPROLINE DEMETHYLASE (EC 1.-.-) (STACHYDRINE
                             SEQUENCE FROM N.A
                                                                      Saccharomycetales;
                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                 YIROO4W OR YIB4W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae; Sinorhizobium.
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                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: FAD (POTENTIAL).
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                                                                                                                                                                                                                                                                            179
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SIMILARITY: TO THE OYE FAMILY OF NADH-DEPENDENT FLAVIN
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13; Conser
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                                                                                                                                                                                                                                                                                                                                 Conservative
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31,
40,
KDA
                                                                       Saccharomycetaceae;
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  ×.
                                                                                                                             Last sequence update)
Last annotation update)
PROTEIN IN BET1-PAN1 INTERGENIC REGION
                                                                                                                                                                       Created)
 Bankier A.T.,
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                                                                                                                                                                                                                                                                                                                                               Score 53.5;
Pred. No. 29;
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RESULT 7
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AC Q9HMN5;
DT 20-AUG-2001
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DT 20-AUG-201
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CO SIGNAL RECOVER
GN SRP54 OR VVIN
OS HALDBACTETIN
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RA SWATTZELIS
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20-AUG-2001 (Rel. 40, 0
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20-AUG-2001 (Rel. 40, 1
        Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Welt D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K. Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL RECOGNITION 54 KDA PROTEIN SRP54 OR VNG2459G.
Halobacterium sp. (strain NRC-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00636; DNAJ_1; 1. PROSITE; PS50076; DNAJ_2; 1.
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SGD; S0001443; YIR004W.
InterPro; IPR001623; DnaJ_N.
Pfam; PF00226; DnaJ; 1.
SMART; SM00271; DnaJ; 1.
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"Nucleotide sequence and analysis of the centromeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145
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X79743; -; NOT_ANNOTA
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12; Conserv
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Lowe T.M., Liang P.,
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KDA PROTEIN (SRP54).
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Pred. No. 28;
8; Mismatches
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(SRP54).
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Ansorge W.;
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SYA_PYRAB SYL...

Q9UY36;
Q9UY36;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Created)
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ProDom; PD000819; SRP54; 1.
PROSITE; PS00300; SRP54; FALSE_NEG
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             This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                           Heilig R.;
                                                                                                                                                                                                                             STRAIN ORSAY;
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NCBI_TaxID=29292;
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Pred. No. 30;
3; Mismatches
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PCNA_SARCR
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MEDLINE-98382535; PubMed=9714841;
MEDLINE-98382535; DubMed=9714841;
Tammariello S.P., Denlinger D.L.;
"Cloning and sequencing of proliferating cell nuclear antigen (PCNA)
"Cloning and sequencing of proliferating cell nuclear antigen (PCNA)
from the flesh fly, Sarcophaga crassipalpis, and its expression in
response to cold shock and heat shock.";
ene 215:425-429(1998).
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15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) (CYCLIN).
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Pfam; PF02272; DHHA1; 1.
Pfam; PF01411; tr.NA-synt_2c; 1.
PRINTS; PR00980; TRNASYNTHALA:
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                            InterPro; IPR000730; PCNA. Pfam; PF00705; PCNA; 1. PRINTS; PR00339; PCNACYCLI
                                                                                                                                                                                                                                                   modified
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                                                                                                            EMBL; AF020427; AAC24238.1; HSSP; P12004; LAXC
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InterPro; IPR002318;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF THE LEADING STRAND.
SUBUNIT: HOMOTRIMER. FORMS A COMPLEX WITH
HETEROPENTAMER IN THE PRESENCE OF ATP (BY
                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: NUCLEAR. SIMILARITY: BELONGS TO THE PCNA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: THIS PROTEIN IS AN AUXILIARY PROTEIN OF DNA POLYMERASE DELTA AND IS INVOLVED IN THE CONTROL OF EUKARYOTIC DNA REPLICATION BY INCREASING THE POLYMERASE'S PROCESSIBILITY DURING ELONGATION
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15; Conserv
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Pred. No. 62;
11; Mismatches
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                                                                                                                                                                                                                                                   is not removed.
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RESULT 11 SUCC_ECOLI

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FR94326;

f 15-JUL-1998 (Rel. 36, Created)
f 15-JUL-1998 (Rel. 36, Last sequence update)
T 20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                  Matches
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PROSITE; PSO0:
DNA-binding; I
DNA_BIND
SEQUENCE 261
                                                                                                                                                                                                                                                   InterPro; IPR003262; Anthr_phosphorbsyltransf.
InterPro; IPR000312; Glycos_transf_3.
InterPro; IPR000053; Flymid_phosphls.
pfam; PP00591; Glycos_transf_3; 1.
ProDom; PD001864; Glycos_transf_3; 1.
ProDom; PD001864; Glycos_transf_3; 1.
ProDom; PD005916; Thymid_phosphls; 1.
Tryptophan biosynthesis; Transferase; Glycosyltransferase.
SEQUENCE 337 AA; 34528 MW; C486203E99E5534E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruykendall L.D., Hunter W.J.;

"The sequence of a symbiotically essential Bradyrhizobium japonicum operon consisting of trpp, trpC and a moac-like gene.";

Biochim. Biophys. Acta 1350:277-281(1997).

-i. CATALYTIC ACTIVITY: ANTHRANILATE + PHOSPHORIBOSYLPYROPHOSPHATE.

-i. CATALYTIC ACTIVITY: NATHRANILATE + PHOSPHORIBOSYLTRANSFERALILATE: PHOSPHORIBOSYLTRANSFERALILATE: PHOSPHORIBOSYLTRANSFERALILATICS OF TRYPOTOPHAN.
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Bradyrhizobium group; Bradyrhizobium.
NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - between Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U79771; AAB39009.1; -
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PS00293;
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                                                                                                                  Conservative
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PCNA_2; 1.
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Pred. No.
                                                                                                                                          Score 51;
Pred. No.
                                                                                                         Pred. No. 33;
3; Mismatches
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SE (EC 2.
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25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97061202; PubMed-8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Aiba H., Baba T., Fujita K., Kashimoto K.,
Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                STRAIN-0157:H7 / RIMD 0509952;

MEDLINB-21156231; PubMed=11258796;

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Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag
Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
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01-APR-1988 (Rel. 07, Last sequence upd
20-AUG-2001 (Rel. 40, Last annotation u
SUCCINVL-COA SYNTHETASE BETA CHAIN (EC
SUCC OR B0728 OR Z0882 OR ECS0753.
                                     STRAIN=K12 / EMG2;
MEDLINE=97443975; PubMed-9298646;
MIDLINE=97443975; PubMed-9298646;
Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed properties
"Comparing the predicted and observed properties
in the genome of Escherichia coli K-12.";
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P07460;
Electrophoresis 18:1259-1313(1997)
                                                                                                                                                                                SEQUENCE OF 1-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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MEDLINE=21074935; PubMed
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"Primary structure of the
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ace 277:1453-1474(1997).
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L., Horiuchi T
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PubMed=11206551;
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M.E., Guest J.R.
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: 6.2.1.5) (SCS-BETA).
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Tobe T.,
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SWISS-2DPAGE; P07460; COLI.
ECOZDBASE; E039, 8; 6TH EDITION.
ECOGENE; EG10981; succ.
InterPro; IPR003135; ATP-grasp.
InterPro; IPR00303; COA_ligase.
Pfam; PF00222; ATP-grasp; 1.
Pfam; PF00549; Ligase-COA; 1.
PROSITE; PS01217; SUCCINYI,_COA_LI
                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                 EMBL; D90711; BAA35394.1; -. EMBL; AE005251; AAG55052.1; -. EMBL; AP002553; BAB34176.1; -.
                                                                                                                                                                                                                                                                 EMBL; J01619; AAA23899.1; -. EMBL; AE000176; AAC73822.1; -. EMBL; D90711; BAA35394.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20092606; PubMed-10625475;
Joyce M.A., Fraser M.E., James M.N., Bridger W.A., "ADP-binding site of Escherichia coli succinyl-CoA revealed by X-ray crystallgraphy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The crystal structure of succinyl-CoA coll at 2.5-A resolution "
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                                                                                                                                                                                                                                                                                                                                                           entities requires a
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Fraser M.E., James M.N., Bridger W.A.,
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MISCELANEOUS: DURING AEROBIC ME:ANDLISM IT FUNCTIONS IN THE
AISCELANEOUS: DURING AEROBIC ME:ANDLISM IT FUNCTIONS IN THE
CITRIC ACID CYCLE, COUPLING THE HYDROLYSIS OF SUCCINYL-COA TO THE
SYNTHESIS OF ATP & THUS REPRESENTS AN IMPORTANT SITE OF
SUBSTRATE-LEVEL PHOSPHORYLATION. IT CAN ALSO FUNCTION IN THE
OTHER DIRECTION FOR ANABOLIC PURPOSES, AND THIS MAY BE
PARTICULARLY IMPORTANT FOR PROVIDIN; SUCCINYL-COA DURING ANAEROBIC
GROWTH WHEN THE OXIDATIVE ROUTE FROM 2-OXOGLUTARRATE IS SEVERELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENZYME REGULATION: EXHIBITS TWO INTERESTING PROPERTIES: "SUBSTRATE SYNERGISM", IN WHICH THE ENZYME IS MOST ACTIVE FOR THE CATALYSIS OF ITS PARTIAL REACTIONS ONLY WHEN ALL THE SUBSTRATE BINDING SITES ARE OCCUPIED, AND "CATALYTIC COOPERATIVITY" BETWEEN ALTERNATING ACTIVE SITES IN THE TETRAMER, WHERERY THE INTERACTION OF SUBSTRATES (PARTICULARLY ATP) AT ONE SITE IS NEEDED TO PROMOTE CATALYSIS AT THE OTHER.
                                                                                                                                          1SCU; 20-APR-95.
2SCU; 02-AUG-99.
1CQI; 10-JAN-00.
1CQJ; 10-JAN-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
MISCELLANEOUS: SUCCINYL-COA SYNTHETASE (SCS) OF E.COI
ITS REACTION VIA THREE STEPS THAT INVOLVE PHOSPHORYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: THE BETA-SUBUNIT SUCCINATE. THE COMPLETE ACTIVE S REGION OF ALPHA- BETA CONTACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: TO OTHER BETA SUBUNITS OF SUCCINYL-COA SYNTHETASES
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                                                                                                                                                                                                                  A24090;
                                                                                                                                                                                                                                                                                                                                         s requires a license agreement (See an email to license@isb-sib.ch).
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 SUCCINYL_COA_LIG_3;
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synthetase
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Q9ZTS1;

20-AUG-2001

20-AUG-2001

20-AUG-2001
                                                                                                                                                                                                             EMBL; L35038; AAB50572.1; ...
InterPro; IPR000567; SBP_bac_1.
Pfam; PF01547; SBP_bacterial_1; 1.
PROSITE; PS01037; SBP_BACTERIAL_1; FALSE_NEG
                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents the statement is not removed.
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P39.
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15-DEC-1998
    PROBABLE
                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                    between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=544
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha Brucellaceae; Brucella.
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                                                                                                                                                                                                        Allergen;
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FUNCTION: ALLERGENIC IN CATTLE.
SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                                                                                                                                                                                                                                                 PROTEIN FAMILY 1.
                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                     ALG--SDTMKQAFDRMSKLRTYVDDNFSGRDWNLASAMVIEGKA
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                                                                                                                                             l Similarity 
15; Conserv
    METHIONYL-TRNA SYNTHETASE
                                                                                                                                                                                                       Transport.
                                                                                                                                                                                               401
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39 KDA PROTEIN.
          (Rel. 40, Created)
(Rel. 40, Last sequence update)
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ALLERGENIC IN CATTLE
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059565;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROTEASOME ALPHA SUBUNIT (EC 3.4.99.46) (MULT
                                      SEQUENCE FROM N.A.
STRAIN-DSM 1825 / TM-1;
MEDLINE=96081920; PubMed=7499378;
Maupin-Furlow J.A., Ferry J.G.;
"A proteasome from the methanogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00133; tRNA-synt_1; 1
Pfam; PF01588; tRNA_bind; 1.
PRINTS; PR01041; TRNASYNTHMET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deniziak M., Mirande M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-:- CATALYTIC ACTIVITY: ATP + L-METHIONINE + TRNA(MET) - AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (Rice). Oryza sativa (Rice). Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                             Archaea; Euryarchaeota; Methanosarcina.
                                                                                                                                                                                                                                                                              COMPLEX ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                      thermophila.";
                                                                                                                                                                       NCBI_TaxID=2210;
                                                                                                                                                                                                                                      Methanosarcina thermophila
                                                                                                                                                                                                                                                                                                                                                                                                                 PSMA_METTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tRNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00178; AA_TRNA_LIGASE_I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF040700; AAC99620.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIGASE) (METRS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity les 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LTNPIDAAIGGSADRNA----EAFDKMKKDDQIAAAMVLR
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SUBCELLULAR LOCATION: CYTOPLASMIC (PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKQGLKSAMGISSDGNAYLQESQFWKLYKEDPAACAVVMK 504
  Chem.
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IPR001412; tRNA-synt_I.
IPR002304; tRNA-synt_met.
IPR002547; tRNA_bind.
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350
353
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                                                                                                                                                                                                                                                                                   SUBUNIT).
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270:28617-28622(1995).
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38
354
353
353
743
89716
                                        the methanogenic archaeon Methanosarcina
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                                                                                                                                                                                                                 Methanosarcinales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A87E8ABBD419D440 CRC64;
                                                                                                                                                                                                                                                                                                     .46) (MULTICATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                               247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Length 804;
                                                                                                                                                                                                                 Methanosarcinaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37
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Query Match
Best Local Similarity
watches 17; Conserve
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ID Y024_MYCPN
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01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
20-AUG-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE GTP-BINDING PROTEIN MG024 HOMOLOG (B01_ORF362).
WHONO26 OR MF128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001353; Proteasome.
InterPro; IPR000426; Proteasome_A.
Pfam; PF00227; proteasome; 1.
PROSITE; PS00388; PROTEASOME_A; 1.
EMBL; AE000015; AAB95776.1;
                                                                                                                                                                                              Nucleic Acids Res. 24:4420-4449(1996).
-i- SIMILARITY: BELONGS TO THE YCHF FAMILY OF GTP-BINDING PROTEINS.
                                                                                                                                                                                                                                    "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.";
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteasome;
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                                                                                                                                                                                                                                                                                            Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                               MEDLINE~97105885;
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-2104;
                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasmataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                             Herrmann R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 TDPSGALLEYKATAIGAGRNAVVEVFEADYKEDMNIEAAILLGMDALYKAAEGKE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TNPIDA-----AIGGSADRNAEAFDKMKKDDQIAAAMVLRGM-----AKDGQF 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: COMPOSED OF TWO SUBUNITS, ALPHA AND BETA. THE COMPLEX FORMED OF FOUR RINGS. THE TWO OUTER RINGS ARE EACH COMPOSED OF SEVEN ALPHA SUBUNITS. THE TWO INNER RINGS ARE EACH COMPOSED OF SEVEN BETA SUBUNITS (BY SIMILATIY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR SLIGHTLY BASIC PH (BY SIMILARITY).

PATHWAY: INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL PROTEOLYTIC PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO PEPTIDASE FAMILY TIA; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEASOME A-TYPE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase;
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                                                                                                                                                                                                                                                                                                               PubMed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
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                                                               Query Match
Best Local :
                                                   Matches
                                                                                                                InterPro; IPR000765; GTP1_OBG.
Pfam; PF01018; GTP1_OBG; 1.
PRLNTS; PR00326; GTP10BG.
GTP-binding; Complete proteome.
NP_BIND 1 75 GTP
NP_BIND 71 75 GTP
SEQUENCE 362 AA; 40607 MW; 70
144 GKIKRKAESGDKQSKEEYQLLAPVLQGLQQN 174
                        12 GSADRNAEAFDKMKKDDQIAAAMVLRGMAKD 42
                                                              Local Similarity
                                                   11;
                                                   Conservative
                                                              21.3%;
                                                                                                                 GTP (POTENTIAL).
GTP (POTENTIAL).
1; 7C79B46CB4D5FF83 CRC64;
                                                               Score 50; DB Pred. No. 48;
                                                   Mismatches
                                                   13;
                                                                          Length 362;
                                                   Indels
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                                                   Gaps
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Search completed: January 10, 2002, 14:09:58

time:

Compugen Ltd

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Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein - protein search, using sw model
    Listing

A_Geneseq_1101:*
1: /SIDSB/gcgdata/
2: /SIDSB/gcgdata
3: /SIDSB/gcgdata
3: /SIDSB/gcgdat
5: /SIDSB/gcgda
6: /SIDSB/gcgda
7: /SIDSB/gcgd
8: /SIDSB/gcgd
9: /SIDSB/gcg
9: /SIDSB/gcg
11: /SIDSB/gc
10: /SIDSB/gc
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length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*

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Copyright (c) 1993 - 2000 Comp
//SIDSB/gcgdata/geneseq/geneseqp/AA1990_DAT:
//SIDSB/gcgdata/geneseq/geneseqp/AA1990_DAT:
//SIDSB/gcgdata/geneseq/geneseqp/AA1990_DAT:
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//SIDSB/gcgdata/geneseq/geneseqp/AA2001_DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

					SUMMARIES	
		æ				
Result No.	Score	Query Match	Query Match Length DB ID	DB.	ID	Description
1	1708	100.0	349	20	AAW95612	Borrelia burgdorfe
N	1695	99.2	349	21	AAB36281	B. garinii P7-1 pr
ω	596	34.9	1328	20	AAY20088	B. burgdorferi ant
4	538.5	31.5	533	20	AAY20112	B. burgdorferi ant
5	437.5	25.6	356	18	AAW22676	Borrelia variable
6	345.5	20.2	156	20	AAY20113	B. burgdorferi ant
7	222	13.0	168	20	AAY20089	B. burgdorferi ant
8	220.5	12.9	738	19	AAW56163	New DNA sequence i
9	214	12.5	681	22	AAB82609	Spider recombinant
10	210.5	12.3	291	22	AAB82608	Spider recombinant
11	208.5	12.2	528	22	. AAB82611	Spider recombinant

ALIGNMENTS

RESULT

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AAW95612
ID AAW9
    New nucleic acid encoding the P39.5 antigen of Borrelia burgdorferi - and related vectors, transformants, antibodies and polypeptides, for diagnosis, prevention and treatment of Lyme disease
                                                                                                                                                                                                                                                            Lyme disease; surface antigen; P39.5; diagnosis; prevention;
vaccine; antisense; therapy; treatment; primer; probe;
                                               WPI; 1999-095676/08.
N-PSDB; AAX07411.
                                                                                 Philipp MT;
                                                                                                         (TULA ) TULANE EDUCATIONAL FUND
                                                                                                                                30-JUN-1997;
                                                                                                                                                      29-JUN-1998;
                                                                                                                                                                             07-JAN-1999.
                                                                                                                                                                                                   WO9900413-A1.
                                                                                                                                                                                                                         Borrelia burgdorferi.
                                                                                                                                                                                                                                                 antibody; DNA.
                                                                                                                                                                                                                                                                                               Borrelia burgdorferi surface antigen P39.5 clone 7-1 polypeptide
                                                                                                                                                                                                                                                                                                                      08-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                             AAW95612;
                                                                                                                                                                                                                                                                                                                                                                   AAW95612 standard; Protein;
                                                                                                                                97us-0051271.
                                                                                                                                                      98WO-US13551.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of a Borrelia burgdorferi surface antigen p39.5 clone 7-1 polypeptide. It can be used in the production of p39.5 or fragments of it which may be used to raise antibodies to, and in the development of vaccines against Lyme disease. The sequence can also be used for making primers and probes for diagnosis, also in DNA vaccines, as antisense therapeutics and for drug screening. Antibodies can be used as diagnostic (immunoassay) reagents, for treating Lyme disease, for affinity purification, for drug screening and to produce anti-idiotype antibodies (used in the
                                                                                                                                                                                                                                                                                                  AAB36281 standard; peptide;
                     Philipp
                                            (TULA ) TULANE EDUCATIONAL FUND
                                                                     28-APR-1999;
                                                                                            25-APR-2000;
                                                                                                                     02-NOV-2000
                                                                                                                                             WO200065064-A1
                                                                                                                                                                   Borrelia garinii.
                                                                                                                                                                                           Lyme
                                                                                                                                                                                                   Variable surface antigen; invariable region; VlsE; Lyme disease;
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                                                                                                                                                                                                                                                     21-FEB-2001
                                                                                                                                                                                                                                                                             AAB36281;
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les 349; Conserv
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                                                                                                                                                                                           borreliosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt ttnadagklfvknagnvggeagdagkaaaavaavsgeqilkaivhaakdggekqgkkaad}
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                                                                    99US-0300971.
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                                                   03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes several peptides comprised of the invariable regions IR1-TR6 of the B. burgdorferi variable surface anti (VISE) variable domain. These peptides can be used in the specific diagnosis, treatment and vaccination against B. burgdorferi, which cau tyme disease (also known as Lyme borreliosis) in humans, dogs, horses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptides comprising an invariable 26-amino acid long region isolated from Borrella burgdorferi (sensu lato), useful for rapid specific diagnosis of lyme disease -
                                                                                                                                                                                                                                    30-DEC-1998
                                                                                                                                                                                                                                                                                       W09859071-A1
                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                          Antigenic protein; vaccine; Lyme disease; infection; detection.
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(HUMA-) HUMAN
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                                                97US-0050359.
97US-0053344.
97US-0053377.
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Best Local Similarity
            Antigenic protein; vaccine;
                                                         19-JUL-1999
                                                                               AAY20112;
                                                                                                     AAY20112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can abe used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caused by
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                                burgdorferi antigenic protein, f49-2.aa.
                                                                                                                         4
                                                                                                                                                           avktaegassgtaaigevv---adaakvadkasvtgiakg 774
                                                                                                                                                                                                    NVGGEAGDAGKAAAAVAAVSGEQILKAIVHAAKD-GGEKQGKKAADRTNPIDAAIGGAGD 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                        akgikeiveaaxgse----klkvaaaxxxnnkeagklfgkagadangdseaaskaagavs 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKGIKGIVDAAGKADAKEGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nnekekaegaikevselldklvtavktaegassgtdaigevvdn---xakxadkasvtgi 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNDHDNHKGTVKNAVDMA-KAAEEAASAASAATGNAAIGDVVKNSGAAAKGGEAASVNGI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999-189980/16
                                                                                                                                                                                                                                                   nahydseaaskaagavsavsgeqilsaivkaageaagdqegkkpeeaknpiaaai---gd
                                                                                                                                                                                                                                                                                                n---aakaadkdsvtgiakgikeiveaaggse----klkvaaakgennkgagklfgkaga 620
                                                                                                                                                                                                                                                                                                                        GDVAKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNAAGAEGTTNADAGKLFVKNAG 195
                                                                                                                                                                                                                                                                                                                                               aaialrgmakdgkfavkkdekgkaegaikgaselldklvkavktaegassgtaaigevvd<sup>.</sup>567
                                                                                                                                                                                                                                                                                                                                                                                           avsgeqilsaivkaaaagaadqdgekpgdaknpiaaaigkgnaddgadfgdgmkkddqia 507
                                                                                                                                                                                                                             NDAAAAFAT--MKKDDQIAAAMVLRGMAKDGQFALKDAAAAH--EGTVKNAVDIIKAAAE 310
                                                                                                                                                                                 AA-SAASAATGSAAIGDVVNGNGATAKGGDAKSVNGIAKG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168;
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                                                                                                    standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 192-193; 275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for the diagnosis, prevention and tre
Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Erwin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1328 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borrelia burgdorferi nucleic acids - used to develop the diagnosis, prevention and treatment of diseases
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                                                        entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 596; DB 20; Pred. No. 2.6e-33; 46; Mismatches 114
          Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MS,
            disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lathigra
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            detection
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es to members
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AAW22676
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Query Match
Best Local S
Matches 157
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22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Page 201-202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated Borrelia burgdorferi nucleic acids - us products for the diagnosis, prevention and treatment caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-SEP-1997;
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    385
                                                                                                                                                                                                                  191
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                                          306
                                                                                                        250 G-GAGDNDAAAAFATMKKDDQIAAAMYLRGMAKDGQFALKDAAAAH---EGTVKNAVDII 305
                                                                                                                                                                                                                                                           211
                                                                                                                                                                                                                                                                                                                                          151 ddqiaaaialrgmakdgkfavkndekgkaegaikgagelldklvkavktaegassgtaai
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                                                                                                                                                                                                                                                                                                                                                                                                                                91 skaagavsavsgeqilsaivkaageaaqdgekpgeaknpiaaaigkgnedgaefkdemkk 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 EAASVNGIAKGIKGIVDAAGKADAKEGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDA 112
                                                                                                                                                                                                             VKNAGNVGGEAGDAGKAAAAVAAVSGEQILKAIVHAA-KDGGEKQGKKAADRTNPIDAAI 249
                                                                                                                                                                                                                                                      gevvaddna-akvadkasvkgiakgikeiveaa.-ggskklkv-aaakeg--nekagklf
                                                                                                                                                                                                                                                                                   GDVVNGDVAKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNAAGAEGTTNADAGKLF
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dklvkavktaegassgtdaigevv-anagaakvadkasvtgiakg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dkasvtgiakgikeiveaaggse----klkvaaaegennekagklfgkagagnagdseaa
                                        KAAAEAA-SAASAATGSAAIGDVVNGNGATAKGGDAKSVNGIAKG
                                                                                 gkgdaengaefnhdgmkkddqiaaaialrgmakdgkfavksgggekgkaegaikgaaell
                                                                                                                                                                     gkvdaahagdseaaskaagavsavsgeqilsaivkaagaaagdqegkkpgdaknpiaaai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erwin AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0057483.
97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 538.5; DB 2
Pred. No. 9.3e-30;
5; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lathigra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94;
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tment of
                                                                                                                                                                                                                                                                                                                                                                                       -----SAATGNAAI 130
    428
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diseases
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                                                                                                                                                                                                                                                                                                                                            210
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                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                    ymp-like sequence (vis) locus consisting of 15 silent vis cassettes (see AxT85043) and the expressed visE gene. Portions of several of the 15 silent vis cassette sequences, located approx. 500 bp upstream of visE, recombine into the central visE cassette region during infection, resulting in antigenic variation and hence immune evasion, long-term survival and pathogenesis in the mammalian host.
                                                                                                                                                                                                                                                                                                                                                       This protein comprises the surface-exposed lipoprotein variable major protein (VMP)-like protein VISE of Borrelia burgdorferi. sequence was deduced from an isolated VISE gene (see AAT85042). sequence was deduced from an isolated vISE gene (see AAT85042) elaborate genetic system has been identified that promotes extensive antigenic variation of VISE. An infectivity related 28-kb linear plasmid, pBB281a, of B. burgdorferi B31 contains a
                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                         Recombinant or native proteins expressed by VMP-like genes, will be useful for the immunotherapy, immunoprophylaxis and immunodiagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding variable major protein-like peptide of Borrelia - useful for recombinant production of VMP like protein or peptide, or for diagnosis of Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barbour AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia burgdorferi strain B31-5A3 (ATCC 35210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Variable major protein-like sequence; VlsE; Lyme disease; relapsing fever;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia variable major protein (VMP)-like protein VlsE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW22676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW22676 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TEXA ) UNIV TEXAS SYSTEM
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                                139
                                                          103
154 daakvadkasvkgiakgikeiveaaggse----klkavaaakgennkgagklfgkagaaa
                                                                                                                                                                                                                Lyme disease, relapsing danimals. They can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1997-435172/40
DB; AAT85042.
                AKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNA-AGAEGTTNADAGKLEVKNAGNV 197
                                                         gkpdstgsvgta
                                                                         GKLDATGAEGTINVNAGKLEVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDV 138
                                                                                                                 al Similarity
127; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 97-99; 130pp; English.
                                                                                                                                                                                      356
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                               They
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                                                                                                                              25.6%;
46.9%;
                                                       Howell JK,
                                                                                                                 26;
                                                                                                                                                                                                                             fever and related disorders in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356
                                                                                                                                                                                                                  be
                                                                                                               Score 437.5; DB 1
Pred. No. 5.6e-23;
6; Mismatches 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VMP-like sequence;
                                                                                                                                                                                                                a Lyme
                                                                                                                                           DB 18;
                                                                                                                 87;
                                                                                                                                                                                                                disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis;
                                                                                                               Indels
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                                                                                                                                          Length
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                                                                                                                                           356;
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KAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNAAGAEGTTNADAGKLFVKNAGNVGG 199

ksqvadkasvtgiakgikeiveaaggse----klkvaaaegennekagklfgkagagnag 57

Query Match Best Local Matches

Local

Similarity

86;

Conservative

17;

Score 345.5; DI Pred. No. 5.2e-7; Mismatches

DB 20; 51;

156; 7;

Indels Length

Gaps

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200

EAGDAGKAAAAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPIDAAIGGAGDNDAAA 259

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RESULT
AAY20113
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                               This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can albe used for detection of members of the Borrelia genus.
                                                       Sequence
                                                                                                                                                                                           Claim 12; Page 202; 275pp; English.
                                                                                                                                                                                                                                  New isolated Borrella burgdorferi nucleic acids - used to develop products for the diagnosis, prevention and treatment of diseases
                                                                                                                                                                                                                                                                            N-PSDB; AAX61810
                                                                                                                                                                                                                                                                                          WPI; 1999-189980/16.
                                                                                                                                                                                                                                                                                                                     Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B. burgdorferi antigenic protein, t49-2.aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY20113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY20113 standard; Protein; 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9859071-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigenic protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-1999
                                                                                                                                                                                                                                                                                                                                                (MEDI-)
                                                                                                                                                                                                                                                                                                                                                            (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 vlgaitg--ligdavs-sglrkvgdsvkaas 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAFA--TMKKDDQIAAAMVLRGMAKDGQFALKDAAAAHEGTVKNAVDIIKAAAEAA--S 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gaefgqdemkkddqiaaaialrgmakdgkfavkd-----gekekaegaikgaaesavrk 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPIDAAIGGAGDNDA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hgdseaaskaagavsavsgeqilsaivtaa-daaeqdgkkpeeaknpiaaai--
                                                                                                                                                                                                                                                                                                                                                             HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                MEDIMMUNE INC.
                                                                                                                                                                                                                      Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                    Erwin AL,
                                                       156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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97US-0050359.
97US-0053344.
97US-0053377.
                                                       AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US12718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine;
20.2%;
                                                                                                                                                                                                                                                                                                                     Hanson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lyme disease; infection; detection
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Best Local Similarity
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22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                            This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can all be used for detection of members of the Borrelia genus.
                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                        Claim 12; Page 193; 275pp; English.
                                                                                                                                                                                                                                                                         New isolated Borrelia burgdorferi nucleic acids - used products for the diagnosis, prevention and treatment of caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                           WPI; 1999-189980/16
                                                                                                                                                                                                                                                                                                                                              Choi GH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigenic protein; vaccine; Lyme disease; infection; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B. burgdorferi antigenic protein, t24-1.aa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY20089 standard; Protein; 168
                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC (MEDI-) MEDIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUN-1998;
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                  349 G 349
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121 g 121
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                                     ekekaegaikevselldklvtavktaegassgtdaigevvdn---xakxadkasvtgiak 120
                                                AAAAHEGTVKNAVDII-KAAAEAASAASAATGSAAIGDVVNGNGATAKGGDAKSVNGIAK 348
                                                                                      EKQGKKAADRTNPIDAAIGGAGDNDAAAAFATMKKDDQIAAAMVLRGMAKDGQFALK--D 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eqdgekpedaknpiaaaigkgngdgaefdqdemkkddqiaaaialrgmakdgkfavkgnn 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dseaaskaagavsavsgeqilsaivkaageaaq-dgekpgeaknpiaaai-gkgnedgae 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFATMKKDDQIAAAMVLRGMAKDGQFALK-DAAAAHEGTVK 299
                                                                                                                                                                                                                                                                                                                AAX61786.
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                                                                                                               Conservative
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97US-0050359.
97US-0053344.
97US-0053377.
                                                                                                                                                              AA;
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                                                                                                                        13.0%;
45.5%;
                                                                                                                                                                                                                                                                                                                                             Hanson MS,
                                                                                                               17;
                                                                                                             Score 222; DB 20;
Pred. No. 1.9e-08;
17; Mismatches 43;
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                                                                                                               43;
                                                                                                                                Length 168;
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diseases
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Query Match 12.9%; Score 220.5; DB 19; Best Local Similarity 29.6%; Pred. No. 1.2e-07; Matches 113; Conservative 29; Mismatches 167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents protein encoded by isolated from Pinctada fucata. The protein be used in cosmetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Pages 9-11; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pinctada fucata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New cDNA and e\cdot g\cdot vector, host cell and polypeptide - used to produce polypeptide in high yields, which is used in cosmetics
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662 gngnggggggggggggggggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 -llrsngasakasakasavastksqiddlkdvlkdlagllkssasasasasasasagggg 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 aaaaaaaaaagggggggggggggagaaaaaaaaaaasasasrqmsgirdalg--dikd
                                                                                                                                               MAKDGQ----FALKDAAAAHEGTVKNAVDIIKAAAEAASAASAATGSAAIGDVV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKLDATGAEGTTNVNAGKL-FVKRAADDGGDA--DDAG-----KAAAAVAASAATGNAA 129
                                                                                               rggdgdgngasavaaaaaaaaaggsaadv....aaaaaaaaamygdgadgpdfdngfgg
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                                                                                                                                                                                                                                            IGG-----AGDNDAAAAFATMKKDDQIAAAMVL-----RG
                                                                                                                                                                                                                                                                                          l----gglgggsaaaaaaaaaasggggralrralrrqmrgg---gsaaaaaaaaaaaa
                                                                                                                                                                                                                                                                                                                                       LFVKNAGNVGGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPIDAA 248
                                                                                                                                                                                                                                                                                                                                                                                       IGDVVNGDVAKAKGGDAASVNGI-AKGIKGIVDAAEKADAKEGKLNAAGAEGTTNADAGK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKAAEEAASAASAATGNAAIGDVVKNSGAAAKGGEAASVNGIAKGIKGIVDAAGKADAKE 78
                                                  -NGNGATAKGGDAKSVNGIAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        738 AA;
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as an
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AAB82609
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Matches 93
                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recovering structural polypeptides in a biological sample, useful for purifying and spinning spider silks and other structural proteins, comprises treating the sample containing the polypeptides with an action comprises treating the sample containing the polypeptides with an action of the polypeptides with a polypeptide with a polypepti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nephila clavipes
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(BUTL/)
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                             1 KNNDHDNHKGTVKNAVD--MAKAAEEAASAASAATGNAAIGDV--VKNSGAAAKGGEAAS 56
2001-483136/52
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) BUTLER M M.
) US SEC OF ARMY.
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1 Similarity 26.6%;
93; Conservative 4
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                                                                                                                                                                                                                                                        681
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                                                                                          ; Score 214; DB; Pred. No. 3e-0
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                                                                                                                       3e-07;
                                                                                                                                                    DB 22;
                                                                                          151;
                                                                                                                                                    Length 681;
                                                                                          Indels
                                                                                       64;
                                                                                       Gaps
                                                                                          15;
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recombinant slik protein, pOE(spl)7. The invention provides methods for purifying and spinning spider silks and other structural proteins. Organic acids are used to lyse recombinant cells or other biological samples (such as non-recombinantly The present sequence is that of orb-weaver spider (Nephila clavipes)

and enrich the purity and yields of

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                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                             Recovering structural polypeptides in a biological sample, useful for purifying and spinning spider silks and other structural proteins, comprises treating the sample containing the polypeptides with an action comprises treating the sample containing the polypeptides with an action comprises treating the sample containing the polypeptides with an action comprises treating the sample containing the polypeptides with an action comprises treating the sample containing the polypeptides with an action comprise treating the sample containing the polypeptides with an action comprise treating the sample containing the polypeptides with an action comprise treating the sample containing the polypeptides with an action comprise treating the sample containing the polypeptides with an action comprise treating the sample containing the polypeptides with an action comprise treating the sample containing the polypeptides with an action containing the polypeptides with a containing the containi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spider; orb-weaver; silk protein; pQE(spl)7; structural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spider recombinant silk protein pQE(spl)7.
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(ARCI/) ARCIDIACONO S.
(BUTL/) BUTLER M M.
(USSA ) US SEC OF ARMY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ion exchange chromatography. Products obtained using the methods of the invention can be used in the construction of many materials including films, fibres, woven articles, sutures, ballistic protection, parachutes and parachute cords. The new method has the following advantages over prior art: it involves fewer steps, requires less time and smaller volumes of reagents, results in better recovery of protein at higher purity (70-99%), is easy to scale up, and the fibres are spun in an environmentally benign solution reducing hazardous waste accumulation and cost.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins by hydrolysing many of the macromolecules while leaving the structural proteins intact. In the case of silk proteins, the resulting lysate is further purified by ion-exchange or affinity chromatography and processed into an aqueous-based mixture for fibre spinning. In the present case, the postspl) gene was closed to contact the postspl of the present case, the postspl of the present case is postspl.
WO200153333-A1
                                                   Misc-difference
                                                                       /note= "encoded by Misc-difference 427
                                                                                                               Location/Qualifiers Misc-difference 417
                                                                                                                                                                                                                     purification; fibre;
                                                                                                                                                                                                                                     Spider; orb-weaver; silk protein; pETNcDS; structural protein;
                                                                                                                                                                                                                                                                       Spider recombinant silk protein pETNcDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGTVKNAVDIIKAAAEAASAASAATGSAAIGDVVNGNGATAKGG
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                                                                                                                                                                                   clavipes
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                                                   /note= "encoded by CGA" 522
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                                                                                                                                                                                                                     spinning
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromatography and processed into an aqueous-based mixture for fibre spinning. In the present case, the princips gene was cloned into vector pET24 for recombinant expression in Escherichia coli, and recombinant silk protein was obtained using formic acid containing denaturant (3 M guanidine-HCl) and by affinity chromatography on nickel-NTA agarose. Products obtained using the methods of the invention can be used in the construction of many materials including films, fibres, woven articles, sutures,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells or other biological samples (such as non-recombinantly derived cells), and enrich the purity and yields of structural proteins by hydrolysing many of the macromolecules while leaving the structural proteins intact. In the case of silk proteins, the resulting lysate is further purified by ion-exchange or affinity resulting lysate is further purified by ion-exchange or affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of the orb-weaver spider (Nephila Clavipes) recombinant silk protein pETNCDS. The invention provides methods for purifying and spinning spider silks and other structural proteins. Organic acids are used to lyse recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ballistic protection, parachutes and parachute cords. The new method has the following advantages over prior art: it involves fewer steps, requires less time and smaller volumes of reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 41-42; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recovering structural polypeptides in a biological sample, useful purifying and spinning spider silks and other structural proteins, comprises treating the sample containing the polypeptides with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tewer steps, requires less time and smaller volumes of reagents, results in better recovery of protein at higher purity (70-99%), is easy to scale up, and the fibres are spun in an environmentally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ARCI/) ARCIDIACONO S. (BUTL/) BUTLER M M. (USSA ) US SEC OF ARMY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-2000; 2000WO-US30086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               benign solution reducing hazardous waste accumulation and cost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-2001
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                                                                                                                                                                   144
                                                                                                                                                                                                                                                                                                148
255 NDAAAAFATMKKDDQIAAAMVLRGMAKDGQFALKDAAAAHEGTVKNAVDIIKAAAEAASA
                                                                                                                                                                                                                                                    84 TGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDVAKAKG 143
                                                                                                                                                                                                                                                                                                                                     24 EAASAASAATGNAATGDVVKNSGAAAKGGEAASVNGTAKGTKGTVDAAGKADAKEGKLDA
                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                         qgagaaaaaaggaggg------gygglgsqgagrgglggggagaaaaaaggagqggygg
                                                                                   VGGEAGDAGKAAAAVAAVSGEQILKAIVHAAKD--GGEKQGKKAADRTNPIDAAIGGAGD
                                                                                                                                                                                                        lggqgagqggyggl----gsqgagrgglggqgagaaaaaggagqgglggqgagaaaaag
                                                                                                                        gagqggygglgsqgagrggqgagaaaaaggagqg---gyggqgagqggygglgsqgagr 314
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                                                                                                                                                  - DAASVNGIAKGIKGIVDAAEKA-DAKEGKLNAAGAEGTTNADAGKLFVKNAGN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       528 AA;
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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27.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 208.5; DB 22; Pred. No. 5.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                       -agqgglggqgagaaaaaaggagqgglggqga
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 528;
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                                       purity. Products obtained using the methods of the invention can be used in the construction of many materials including films, fibres, woven articles, sutures, ballistic protection, parachates and parachate cords. The new method has the following advantages over prior art: it involves fewer steps, requires less time and smaller volumes of reagents, results in better recovery of protein at higher purity (70-99%), is easy to safe, and the fibres are
                                                                                                                                                                                                                                                                                                                                   proteins by hydrolysing many of the macromolecules while leaving the structural proteins intact. In the case of silk proteins, the resulting lysate is further purified by ion-exchange or affinity chromatography and processed into an aqueous-based mixture for fibre spinning. In the present case, the pET((SP1)4/(SP2)1)4 gene was cloned into vector pET24 for recombinant expression in Escherichia coli, and recombinant silk protein was obtained in 75-75% purity using propionic acid and anion-exchange chromatography on QAE-Sephadex A50. When denaturant (3 M guanidine-HCl) was added
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of orb-weaver spider (Nephila clavipes) recombinant silk protein pET((SP1)4/(SP2)1)4. The invention provides methods for purifying and spider silks and other structural proteins. Organic acids are used to lyse recombinant cells or other biological samples (such as non-recombinantly derived cells), and enrich the purity and yields of structural
                                                                                                                                                                                                                                                                                                             t o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 38-40; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recovering structural polypeptides in a biological sample, useful for purifying and spinning spider silks and other structural proteins, comprises treating the sample containing the polypeptides with an acid
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structural protein; purification; fibre; spinning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spider recombinant silk protein pET((SP1)4/(SP2)1)4.
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accumulation and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mello
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MELL/) MELLO C M.
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                                                                                                                                                                                                                                                                      the propionic acid, the recombinant protein was obtained in 80 rity. Products obtained using the methods of the invention can
                                in an environmentally benign solution
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) BUTLER M M.
) US SEC OF ARMY.
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                            hazardous waste
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                                                                Disclosure; Page 106-108; 168pp; English
                                                                                                       New synthetic variants of spider dragling protein - for making fibres useful as clothing, surgical silk, plastic reinforcement
                                                                                                                                               WPI; 1995-036479/05
                                                                                                                                                                         Fahnestock SR;
                                                                                                                                                                                                                            15-JUN-1993;
                                                                                                                                                                                                                                                     15-JUN-1994;
                                                                                                                                                                                                                                                                                                        W09429450-A2
                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                          DP-1A analogue; fibre; rope; surgical suture;
                                                                                                                                                                                                                                                                                                                                                                                                Spider; dragline protein; variant;
                                                                                                                                                                                                                                                                                                                                                                                                                           Spider dragline variant, DP-1B.16 polymer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR99057;
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                                                                                                                                                                                                  (DUPO ) DU PONT
                                                                                                                                                                                                                                                                                                                                                          Spider; dragline protein; variant; monomer; polymer; fibre forming region; Spidroin 1; Nephila clavipes; DP1; mimic; DP-1A analogue; fibre; high tensile strength; elasticity; cloth prope; surgical suture; implant; reinforcement; film; coating.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAASAATGSAAIGDV--VNGNGATAKGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAGNYGGEAGDAGKAAAAYAAYSGEQILKAIYHAAKDGGEKQGKKAADRTNPIDAAIGGA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDVAKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNAAGAEGTTNADA----GKLEVK 192
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                                                                                                                                                                                                  DE NEMOURS & CO
                                                                                         DNA,
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27.4%;
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                                                                                           vectors and
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Pred. No. 9.2e-07;
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                                                                                                                                                                                                                                                                                                                                                                        clothing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
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This sequence represents a synthetic spider dragline variant polymer. DP-1B.16. The sequence of the DP-1B.16 monomer is given in AAR99056. The polypeptide monomer is a variant based on a consensus sequence derived from the fibre forming regions of spider dragline protein,

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RESULT 1
AAR99055
ID AARS
XX
XX
AC AARS
AC AARS
XX
DT 17-2
XX
DE Spic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC or Bacillus subtilis. Synthetic analogues of DPI were designed to mimic the repeating consensus sequence of the natural protein and the pattern CC of variation among individual repeats. This monomer exhibits all of the CC regularities of (1), (5) below. In addition, it exhibits a regularity of the natural sequence which is not shared by DP-1A, namely that a repeat CC in which both GYG and GRG are deleted is generally preceded by a repeat CC lacking the entire poly-alanine repeat, with one intervening repeat. CC The sequence of DP-1B matches the natural sequence more closely over CC a more extended segment than does DP-1A. The individual repeats differ CC from the consensus sequence given in AAW06201 according to the pattern: CC (1) the poly-alanine sequence varies in length from 0-7 CC (3) aside from the entire poly-alanine sequence is deleted, CC (3) aside from the poly-alanine sequence, deletions usually CC encompass integral multiples of three consecutive residues; (4) deletion of GYG is generally accompanied by deletion of GRG in the server serior and consecutive residues;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the same sequence; and
(5) a repeat in which the entire poly-alanine sequence is
aclassed is generally preceded by a repeat containing six alanine
                   Spider dragline variant, DP-1B.9 polymer
                                                                    17-JAN-1997
                                                                                                                                                            AAR99055 standard; Protein; 606 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The proteins may be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films, coatings, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          esp. the natural protein 1 (Spidroin 1) from Nephila clavipes. ONA sequence encoding the monomer may be used in the recombinant production of the variant protein in a recombinant host, e.g. E.
                                                                                                                                                                                                                                                                       575 sqgagrggqgagaaaaaaggagqg 598
                                                                                                                                                                                                                                                                                                                     326 DVVNGNGATAKGGDAKSVNGIAKG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 qgagqggygglgsqgagrgglggqgagaaaaaaaggagqgglgsqgagagaaaaaagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133
                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 agqggygglgsqgagr-----ggqgagaaaaaaggagqggygglgsqgagqggyggl 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 -----qggygglgsqg-----agr------gg----lggqgagaaaaaaaggagqgg 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 sqgagqgagaaaaaaggagqggygglgsqgagrggqgagaaaaaaggagggygglgsgag 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 AKAAEEAASAASAATGNA-----AIGDVVKNSGAAAKGGEAASVNGIAKGIKGIVDAAG 72
                                                                                                                                                                                                                                                                                                                                                               gsqgagrgglggqgagaaaaaaaggagqgglg-sqgagqgagaaaaaaggagqggygglg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKQ-----GKKAADRTNPIDAAIGGAGDNDAAAAFATMKK-----DDQIAAAMVLRGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVNGDVAKAKGGDAASVNGTAKGTKGTVD------AAEKADAKEGKLNAAGA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KADAKEGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAAVAASAATGNAAIGD 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lgsqgagqagaaaaaaggagqgygglgsqgagrggqgagaaaaaaggagqggygglgs 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGTTNADAGKLFVKNAGNVGGEAGDAGKAAAAVAAVSGEQIL-----KAIVHAAKDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          ----GQFALKDAAAAHEGTVKNAVDIIKAAAEAASAASAATGSA-----AIG
                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.9%;
26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 203.5;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162;
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Matches
                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or Bacillus Subtilis. Synthetic analogues of DPI were designed to mimic the repeating consensus sequence of the natural protein and the pattern of variation among individual repeats. This monomer exhibits all of the regularities of (1)-(5) below. In addition, it exhibits a regularity of the natural sequence which is not shared by DP-1A, namely that a repeat in which both GYG and GRG are deleted is generally preceded by a repeat lacking the entire poly-alanine repeat, with one intervening repeat. The sequence of DP-1B matches the natural sequence more closely over a more extended segment than does DP-1A. The individual repeats differ from the consensus sequence given in ARMO6201 according to the pattern: (1) the poly-alanine sequence varies in length from 0-7 residues; (2) when the entire poly-alanine sequence is deleted, so also is the surrounding sequence encompassing AGRGGLGGGAAANGG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a synthetic spider dragline variant polymer, DP-1B.9. The sequence of the DP-1B.9 monomer is given in AAR99054. The polypeptide monomer is a variant based on a consensus sequence derived from the fibre forming regions of spider dragline protein, esp. the natural protein 1 (Spidroin 1) from Nephila clavipes. The
                                                                                                                                                                                                                                                                 The proteins may be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films, coatings, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spider; dragline protein; variant; monomer; polymer; fibre forming region; Spidroin 1; Nephila clavipes; DDP; mimic; DDP-1A analogue; fibre; high tensile strength; elasticity; cloth rope; surgical suture; implant; reinforcement; film; coating.
                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                       deleted is
                                                                                                                                                                                                                                                                                                                                                                                              in the same sequence; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence encoding the monomer may be used in the recombinant production of the variant protein in a recombinant host, e.g. E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 88-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-036479/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09429450-A2
  76
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                                                                                                                                           Local Similarity
AKEGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVN 135
                                    AASAASAATGNAAIGDVVKNSGAAAKGGEAASVNGIAKGIKGIV------DAAGKAD 75
                                                                                                                          101;
                                                                                                                                                                                                                                                                                                                                                                                                           (3) aside from the poly-alanine sequence, deletions usually
ss integral multiples of three consecutive residues;(4) deletion of GYG is generally accompanied by deletion of
                                                                                                                                                                                                                                                                                                                                                     (5) a repeat in which the entire poly-alanine
is generally preceded by a repeat containing s
                                                                                                                                                                                                                             606 AA;
                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US06689
                                                                                                                                       11.9%; Score 203.5; DB 1 26.5%; Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168pp; English.
                                                                                                                          32;
                                                                                                                          Mismatches
                                                                                                                                                              DB 16;
                                                                                                                          183;
                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                     sequence is
six alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clothing;
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RESULT 15
AAY40101
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                                                                  The present sequence represents a polymer of an analogue of the spider silk protein spidroine major 1. The protein improves the moisturizing/ softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions have use as hair or skin care products; and make-up or sunscreens. As the protein is a good, persistent film-formers on the skin of low surface density, it can be used for delivery of active agents that are generally difficult to administer, e.g. vitamins,
                                          hormones, mois
skin and hair.
                                                                                                                                                                                                             Claim 8; Fig
                                                                                                                                                                                                                                       Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens \,\cdot\,
                                                                                                                                                                                                                                                                                       WPI; 1999-510729/43.
                                                                                                                                                                                                                                                                                                                    Philippe M,
                                                                                                                                                                                                                                                                                                                                                                                 11-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                             11-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
Nephila clavipes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spider silk protein; spidroine major 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscreen; hormone; moisturizer; skin disorder; skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymer of an analogue of spider silk protein spidroine major 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY40101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY40101 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                 (OREA ) L'OREAL SA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNADAGKLEVKNAGNVGGEAGDAGKAAAAVAAVSGEQIL------KAIVHAAKDGGEKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gagrgglggqgagaaaaaaggagqgglg-sqgagqagaaaaaaggagqggygglgsqg 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \tt qgagqgagaaaaaaggagqggygglgsqgagagaaaaaaggagqggygglgsqga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GKKAADRTNPIDAAIGGAGDNDAAAAFATMKK-----DDQIAAAMYLRGMAKD
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                                                          moisturizers
                                                                                                                                                                                                                                                                                                                    Garson JC,
                                                                                                                                                                                                          5B; 32pp; French.
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1..101
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                                                     or agents for treating disorders of the
                                                                                                                                                                                                                                                                                                                    Arraudeau
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                                                                                                                                                                                                                                                                                                                    JP;
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Sequence

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Best Local
378 agrggggagaaaaaaggaggg
                                    329
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                                                                                                                          ggygglgsqgagr-----ggqgagaaaaaaggagqggygglgsqgagqggygglgsq
                                                               gagrgglggqgagaaaaaaggagqgglg-sqgagqgagaaaaaaggagqggygglgsqg
                                                                                                ------GQFALKDAAAAHEGTVKNAVDIIKAAAHAASAASAATGSA-----AIGDVV
                                                                                                                                                                                                                                                                                          GDVAKAKGGDAASVNGIAKGIKGIVD------AAEKADAKEGKLNAAGAEGT 181
                                                                                                                                                                                                                                                                                                                        agaaaaaaaggagggglgsqgagqagaaaaaaggugqggygglgsqgagrgggggagaaa 86
                                 NGNGATAKGGDAKSVNGIAKG 349
                                                                                                                                                                                           9q9gygglgsqgagrgglggqgagaaaaaaaggagqgglgsqgagqgagaaaaaggagq
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                                                                                                                                                                                                                                                                                                                                                         AKEGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVN 135
                                                                                                                                                               -----GKKAADRTNPIDAAIGGAGDNDAAAAFATMKK-----DDQIAAAMVLRGMAKD
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26.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 203.5; DB 20;
Pred. No. 1.4e-06;
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Job time: 168 sec January 10, 2002, 14:05:14

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Result
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-09-247-806-1
US-08-425-069-2
US-09-34-177-3
US-08-209-747-2
US-08-209-747-2
US-08-209-747-2
US-09-247-806-4
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US-09-247-806-4
US-07-941-523-2
US-08-478-029A-36
US-08-478-029A-36
US-08-478-029A-36
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PCT-US94-0776-16
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	1, Appl	 Appl 	64, Appl	35, Appl	4, Appl		31, Appl			 Appl: 		89, Appi		88, Appl	App.	88, Appl	53, Appl

ALIGNMENTS

US-08-864-038A-3

Sequence 3, Application US/08864038A Patent No. 6001592 GENERAL INFORMATION:

RESULT

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MEDLIN TYPE: Diskette, 3.50 inch, 1.44
COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,038A
FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-184459
FILING DATE: 15-July-196
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REGISTRATION NUMBER: 5-5610
TELECOMMUNICATION INFORMATION:
mer Penioner (712)486-2340
                                                                                                                                                                                                                                                          INFORMATION FOR SEQ
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ZIP: 514-01
COMPUTER READABLE FORM:
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TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBOD
TITLE OF INVENTION: TO SAID POLYPEPTIDE
UMMBER OF SEQUENCES: 4
                                                                   FEATURE:
                                                                                                                             MOLECULE TYPE: |
ORIGINAL SOURCE:
                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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ADDRESSEE: 812-5 Hirano
                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Isshing
CITY: Tsu-city
STATE: Mie-pre
                      NAME/KEY:
LOCATION:
                                                                                     CELL TYPE:
                                                                                                         ORGANISM:
IDENTIFICATION METHOD:
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(by experiment)
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US-08-864-038A-3

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GENERAL INFORMATION:

APPLICANT: PHILLIPPE, Michel

APPLICANT: GARSON, Jean-Claude

APPLICANT: GARSON, Jean-Pierre

TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT

TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN

TITLE OF INVENTION: ANALOG

TRENT APPLICATION NUMBER: US/09/247,806

CURRENT APPLICATION NUMBER: US/09/247,806

EARLIER APPLICATION NUMBER: FR 98/01614

EARLIER APPLICATION NUMBER: FR 98/01614

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 606
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                                                                                                                                                                                                                                                                              ; TYPE: PRT; ORGANISM: Nephila clavipes US-09-247-806-6
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US-09-247-806-6
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Best Local Similarity
Matches 102; Conserv
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Best Local Similarity 29.6
Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                553 GGGWGGGMGGGFGVGLGGGFGGGGSSAAAAAAAA-----AAAAGFGGGGRRGRGRG 605
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                   76 AKEGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAATGDVVN 135
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                                                                                                                    25 AASAASAATGNAAIGDVVKNSGAAAKGGEAASVNGIAKGIKGIV-----DAAGKAD 75
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                                                                                                                                                                12.1%; Score 207.5; DB 4; 26.8%; Pred. No. 2.3e-10; tive 32; Mismatches 182;
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Query Match 11.9%; Score 203.5; DB 4; Length 604; Best Local Similarity 26.6%; Pred. No. 5.2e-10; Matches 102; Conservative 35; Mismatches 162; Indels 85; Ga	LENGTH: 604 amino acids TYPE: amino acid STRANDEDNESS: unknown TOPOLOGY: unknown MOLECULE TYPE: protein -556-978B-63		REGIST FLOTO, DANGER AND REGIST REGISTRATION NUMBER: CR-9389-A REFERENCE/DOCKET NUMBER: CR-9389-A	G DATE: JUNE 15, 1993 Y/AGENT INFORMATION:	ON: 435 ION DATA:	APPLICATION NUMBER: US/08/556,978B FILING DATE:	OPERATING SYSTEM: MICROSOFT WINDOWS 95 SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 CHIBERT ADDITATION DATA:	MEDIUM TYPE: DISKETTE, 3.50 INCH COMPUTER: IBM PC COMPATIBLE	COUNTRY: UNITED STATES OF AMERICA ZIP: 19898 COMPUTED PEADABLE FORM:	ILMINTON DELAWARE	CORRESPONDENCE ADDRESS: ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET	OF INVENTION: SPI	APPLICANT: FAHNESTOCK, STEPHEN F. TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED	SULT 3 3-08-556-978B-63 Sequence 63, Application US/08556978B GENERAL TURGORANTION:	580 AGRGGQGAGAAAAAAGGAGQG 600	329 NGNGATAKGGDAKSVNGTAKG 349	521 GAGRGGLGGQGAGAAAAAAAGGAGQGGLG-SQGAGQGAGAAAAAAGGAGQGGYGGLGSQG	283AIGDVV	469 GGYGGLGSQGAGRGGQGAGAAAAAAGGAGQGGYGGLGSQGAGQGGYGGLGSQ	235GKKAADRTNPIDAAIGGAGDNDAÄAAFATMKKDDQIAAAMVLRGMAKD	102 IRDINORUF YARNONYOGENOURARAKANYANYOEQLID FARIYORAKIODERAY INTERNATIODERAY IN	49 QGAGQGAGAAAAAAGGAGQGGYGGLGSQGAGRGGQGAGAAAAAAGG
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RESULT 4
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Query Match
Best Local Similarity
                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/077,600
APPLICATION NUMBER: 08/077,600
FILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXMETHY
REGISTRATION NUMBER: 35,692
REFERENCE/DOCKET NUMBER: CR-9389-A
TELEPHONE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                              TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: MICROSOFT WORD FOR WINDOWS CURRENT APPLICATION DATA:
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MEDIUM TYPE: DISKETT
                                                                                         MOLECULE TYPE:
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ADDRESSEE: E. I. DU
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                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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CITY: WILMINTON
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                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNITED STATES OF AMERICA
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26.5%;
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 Score 203.5; DB 4
Pred. No. 5.2e-10;
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              DB 4;
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US-09-247-806-8
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US-09-247-806-8
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Patent No. 6280747
                                                                                                                                                                                                                                                                              Matches 101;
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                                                                                                                                                                                                                                                                                                                   Query Match
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APPLICANT: GARSON, Jean-Claude
APPLICANT: ARRAUDEAU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6388-0365-0
CURRENT APPLICATION NUMBER: US/09/247,806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER FILING DATE: 1998-02-11 NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 1999-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
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                                                                            136 GDVAKAKGGDAASVNGIAKGIKGIVD----
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                                                                                                                                                                                                                                                                                                  Local Similarity
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                                       QGAGQGAGAAAAAAGGAGQGGYGGLGSQGAGRGGQGAGAAAAAAAGGAGQGGYGGLGSQGA 204
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                                                                                                                   AAAGGAGQGGYGGLGSQGAGQGGYGGLGSQGAGGAGAAAAAAAAAGGAGQGGLGS
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                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,60
PILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Cent no. 6268169
GENERAL INFORMATION:
APPLICANT: FAHNESTOCK, STEPHEN F.
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INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
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COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE,
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acid
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APPLICATION NUMBER: US/08/556,978B
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294 GQGGYGGLGSQGAGRGGLGGQGAGAAAAGGAGQGGLGGQGAGQGAGAAAAAAGGAGQGGY 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 AGRGGQGAGAAAAAAGGAGQG 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 GGYGGLGSQGAGR-----GGQGAGAAAAAAGGAGQGGYGGLGSQGAGQGGYGGLGSQ 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205
                                74 ADAKEGKIDATGA--EGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASA----- 123
                                                                                                               20 KAAEEAASAASAATGNAAIGDV-VKNSGAAAKGGE-----AASVNGIAKGIKGIVDAAGK 73
                                                                                                                                                              Local Similarity
les 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1007 MA
CITY: WILMINTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MICROSOFT WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                            QGAGQGAGASAAAAGGAGQGGYGGLGSQGAGRGGEGAGAAAAAAGGAGQGGYGGLGGQGA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGNGATAKGGDAKSVNGIAKG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGRGGLGGQGAGAAAAAAAAGGAGQGGLG-SQGAGQGAGAAAAAAAGGAGQGGYGGLGSQG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------GQFALKDAAAAHEGTVKNAVDIIKAAAEAASAASAATGSA-----AIGDVV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQGGYGGLGSQGAGRGGLGGQGAGAAAAAAAGGAGQGGLGSQGAGQGAGAAAAAAGGAGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DELAWARE
                                                                                                                                                                                                                                                                                                                                                           651 amino acids
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                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                        unknown
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                                                                                                                                                        11.5%; Score 197; DB 4; Length 65 26.1%; Pred. No. 2.1e-09; tive 32; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08/077,600
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                                                                                                                                                                                               Length 651
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                                                                                                                                                          Gaps
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APPLICANT: PHILLIPPE, Michel
APPLICANT: GARSON, Jean-Claude
APPLICANT: GARSON, Jean-Claude
APPLICANT: GARSON, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6388-0365-0
CURRENT APPLICATION NUMBER: US/09/247,806
CURRENT PILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: FR 98/01614
EARLIER APPLICATION NUMBER: FR 98/01614
SOFTWARE: PATENTIAL DATE: 1998-02-11
VOMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIAL OF SEQ ID NOS: 14
SOFTWARE: PATENTIAL OF SEQ ID NOS: 14
SOFTWARE: PATENTIAL OF SEQ ID NOS: 14
SOFTWARE: DATE: 1998-02-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.5%; Score 197; DB 4; Best Local Similarity 26.1%; Pred. No. 2.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
  511
                                           274 MYLRGMAKDGQFALKDAAAAHEGTYKNAYDIIKAAAEAASAASAATGSAAIGDYYNGNGA 333
                                                                                                459
                                                                                                                                                                                                410
                                                                                                                                                                                                                                                171
                                                                                                                                                                                                                                                                                           354 GGLGSQGAGRGGLGGQGAGAVAAAAAGGAGQGGYGGLGSQGAGRGGQG----AGAAAAAA 409
                                                                                                                                                                                                                                                                                                                                              124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 QGAGQGAGASAAAAGGAGQGGYGGLGSQGAGRGGFGAGAAAAAAAGGAGQGGYGGLGGQGA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         511 --- QGAGQGGYGGLGSQGSGRGG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    410
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                                                                                                                                                                                                                                                                                                                                                                                                                                         74 ADAKEGKLDATGA--EGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 KAAEEAASAASAATGNAATGDV-VKNSGAAAKGGE-----AASVNGIAKGIKGIVDAAGK 73
---QGAGQGGYGGLGSQGSGRGG------LGGQGAGAAAAAAGGAGQGGLGGQGAG
                                                                                             AGRGGQGAA-----AAAGGAGQGGYGGLGSQGAGRGGQGAGAAAAAAVGAGQEGIRG- 510
                                                                                                                                                GEKQGKKAADRTNPIDAAIGGAGDN-----
                                                                                                                                                                                             GGAGQRGYGGLGNQGAGR----GGLGGQG--AGAAAAAAAGGAGQGGYGGL---GNQG
                                                                                                                                                                                                                                           GKLNAAGAEGTTNADAGKLFVKNAGNVGGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDG
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                                                                                                                                                                                                                                                                                                                                           -----ATGNAAIGDVVNGDVAKAKGGDAA-----SVNGIAKGIKGIVDAAEKADAKE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGQRGYGGLGNQGAGR-----GGLGGQG--AGAAAAAAAGGAGQGGYGGL---GNQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --LGGQGAGAAAAAAGGAGQGGLGGQGAG
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                                                                                                                                             ----DAAAAFATMKKDDQIAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
231 GEKQGKKAADRTNPIDAAIGGAGDN---
                                                                                                 171
                                                                                                                                                                                                             294 GQGGYGGLGSQGAGRGGLGGQGAGAAAAGGAGQGGLGGQGAGAGAAAAAAGGAGQGGY 353
                                                                                                                                                                                                                                                                                         234 QGAGQGAGASAAAAGGAGQGGYGGLGSQGAGRGGEGAGAAAAAAGGAGQGGYGGLGGQGA 293
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STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                      74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                              20 KAAEEAASAASAATGNAAIGDV-VKNSGAAAKGGE-----AASVNGIAKGIKGIVDAAGK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                  ADAKEGKLDATGA--EGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASA----- 123
                                                         GGAGQRGYGGLGNQGAGR----GGLGGQG--AGAAAAAAAGGAGQGGYGGL---GNQG
                                                                                             GKLNAAGAEGTTNADAGKLFVKNAGNVGGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDG 230
                                                                                                                                    GGLGSQGAGRGGLGGQGAGAVAAAAAAGGAGQGGYGGLGSQGAGRGGQG----AGAAAAAA 409
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                                                                                                                                                                       ---ATGNAAIGDVVNGDVAKAKGGDAA-----SVNGIAKGIKGIVDAAEKADAKE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Birch, Stewart, Kolasch & 301 No. 5728810th Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  718 amino acids
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lewis, Randolph V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISOLATED DNA CODING FOR SPIDER SILK PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CONTAINING THE ISOLATED DNA, AND PRODUCTS THERE
                                                                                                                                                                                                                                                                                                                                                                  11.5%; Score 197; DB 1; 26.1%; Pred. No. 2.4e-09; tive 32; Mismatches 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2:
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Street
                                                                                                                                                                                                                                                                                                                                                                    164;
                    -DAAAAFATMKKDDQIAAA 273
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US-08-317-844B-2
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Best Local
                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING STULE...

SOFTWARE: Patentin Release #1.u, ve CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: USCOB/317,844B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY JT., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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   171
                                     354
                                                                        124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                            74 ADAKEGKLDATGA--EGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASA------ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: .U
ZIP: 22046
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STATE: Virginia
                                                                                                                                                                                                                                                                     Local
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GKLNAAGAEGTTNADAGKLFVKNAGNVGGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDG 230
                                     GGLGSQGAGRGGLGGQGAGAVAAAAAGGAGQGGYGGLGSQGAGRGGQG----AGAAAAAA 409
                                                                                                            GQGGYGGLGSQGAGRGGLGGQGAGAAAAGGAGQGGLGGQGAGQGAGAAAAAAGGAGQGGY 353
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                                                                                                                                                                                                                                                                                                                                                                                                                       718 amino acids
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(703) 241-2848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lewis, Randolph V.
                                                                                                                                                                                                                                                                                                                                                              protein
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                                                                                                                                                                                                                                                                     11.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28,977
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Best Local S
                                                                      Matches
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APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Neil C.
TITLE OF INVENTION: HUMAN FIBROUS PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS.
                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 747 amino acids
                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPHONE: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US
FILING DATE: HEREWITH
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ent No. 6127146
                                                                                                                                                    LIBRARY: Genuc.
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234 QGAGQGAGASAAAAGGAGQGGYGGLGSQGAGRGGEGAGAAAAAAAGGAGQGGYGGLGGQGA 293
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OPERATING SYSTEM:
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                    20 KAAEEAASAASAATGNAAIGDV-VKNSGAAAKGGE-----AASVNGIAKGIKGIVDAAGK 73
                                                                                                                                                                                                                TYPE: sin
                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
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CITY: Palo Alto
                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
                                                                                                                                                                                                                                     single
                                                               11.5%; Score 197; DB 3;
26.1%; Pred. No. 2.5e-09;
tive 32; Mismatches 164
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    LGGQGAGAAAAAAGGAGQGGLGGQGAG

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US-08-209-747-2
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                                                                                                                                                                                                                                                    TELEPHONE: 703-205-80
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                     FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: N.
                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                     FEATURE:
                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Colgin, Mark
TITLE OF INVENTION: CDNAs Encoding Minor Ampullate
TITLE OF INVENTION: Silk Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lewis, APPLICANT: Colgin,
                                                                                                                             TYPOTHETICAL:
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                                                  TISSUE TYPE: minor ampullate gland
                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 14-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: P.O. Box 7.
CITY: Falls Church
STATE: Virginia
NAME/KEY:
                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/209,747 FILING DATE: 14-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22040-3487
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O. Box 747
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Matches
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                          TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                          REFERENCE/DOCKET NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 1447-104P

TELEPHONE: 703-205-8000

TELEPHONE: 703-205-8000

TELEPAX: 703-205-8000
                                                                                                                                                                                                                                                      CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
TITLE OF INVENTION: CDNAS Encoding Minor Ampullate Spider
TITLE OF INVENTION: Sik Proteins
                                                                                                                                                                                            FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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les 97; Conserv
                                                                                                                                                         NAME: Murphy Jr., Ge REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 AKEGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGK----AAAAVAASAATGNAAI 130
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                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/209,747
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T: P.O. Box 747
Falls Church
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US-08-556-978B-21

; Sequence 21, Application US/08556978B

; Patent No. 6568169
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ORGANISM: N. clavipes
TISSUE TYPE: minor ampullate gland
                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FAHNESTOCK, STEPHEN F.
TITLE OF INVENTION: NOVEL RECOMBINANTLY
TITLE OF INVENTION: SPIDER SILK ANALOGS
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ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE: JUNE 15,
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
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                                                                                                                                                                                                                                                                                                                    STREET: 1007 MA
CITY: WILMINTON
STATE: DELAWARE
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                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76
                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKNAGNVGGEAG-DAG-KAAAAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPIDAA 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGGAGDNDAAAAFATMKKDDQIAAAMVLRGMAKDGQFALKDAAAAHEGTVKNAVDIIKAA 308
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                                                                                                                                                                                                                                                                                                      UNITED STATES OF AMERICA
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28.4%;
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Pred. No. 3.2e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRODUCED
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REFERENCE/DOCKET NUMBER: CR-TELECOMMUNICATION INFORMATION: TELEPHONE: 302-892-8112 TELEPHAX: 302-773-0164

CR-9389-A

21:

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FILE REFERENCE: 6388-0365-0
CURRENT APPLICATION NUMBER: US/09/247,806
CURRENT FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: FR 98/01614
EARLIER FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 606
TYPE: PRT
ORGANISM: Nephila clavipes
US-09-247-806-4
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  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09247806 Patent No. 6280747
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
SEQUENCE: 606 amino acids
                                                                                                                                                                                                                                                                                                         APPLICANT: GARSON, Jean-Claude
APPLICANT: ARRAUDEAU, Jean-Plerre
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PHILLIPPE, Michel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GA-----BGTTNVNAGKLFVKRAADDGG----DADDAGKA-----AAAVAASAATGNAA 129
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26.4%; Pred. No. 3.1
    11.48;
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  Score 194.5;
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RESULT 15
US-07-941-523-24
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; MOLECULE TYPE: US-07-941-523-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 26.4 Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                           FILING DATE: 19920908
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: BNL9
TELECOMMUNICATION INFORMATION:
                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDLIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT application Data:
APPLICATION NUMBER: US/07/941,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Barbour, Alan G
TITLE OF INVENTION: Cloning and Expression
TITLE OF INVENTION: Lipoproteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dunn, John J
APPLICANT: Barbour, Ala
                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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ZIP: 01730
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                                     STRANDEDNESS:
TOPOLOGY: 11
                                                                        TYPE: AMINO ACID
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                                                                                                                                                          (617) 861-6240
(617) 861-9540
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1; Mismatches 176;
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Search completed: January 10, 2002, 14:03:56 Job time: 90 sec
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                                                                                                                                                                                                                                                             293 AHEGTVKNAVDIIKAAAEAASAASAATGSAAIGDVVNGNGATAKGGDAKSVNGIAK 348
                                                                                                 273 -----SLVKTGKLAAGAADNATGG---GKEVQGVGVAAANKLLRAVEDVIK 315
                                                                                                                                                                              225 SGEN-----DAQLAAAADGNTSAISFAKGGSDAHLAGANTPKAAAVAGGIALR---- 272
                                                                                                                                                                                                          234 QGKKAADRTNPIDAAIGGAGD-NDAAAAFATMKKDDQIAAAMVLRGMAKDGQFALKDAAA 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 MAKAAEEAASAASAATGNAAIGDVVKNSGAAAKGGEAASVNGIAKGIKGIVDAAGKADAK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 E----GKLDATGAE-GTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAA----- 124
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Maximum Match 100%
Listing first 45 summaries
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Pending_Patents_AA_Main:*

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6: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
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   /cgn2_6/ptodata/2/paa/US60_COMB.pep:*
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524.306 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result		Query				
No.	Score	Match Length DB	Length		ID	Description
1	1708	100.0	349	18	US-09-445-803-2	Sequence 2, Appli
N	1702	99.6	349	17	US-09-300-971A-9	Sequence 9, Appli
ω	532	31.1	323	17	US-09-300-971A-11	Sequence 11, Appl
4	480	28.1	189	17	US-09-300-971A-10	Sequence 10, Appl
5	437.5	25.6	356	_	PCT-US97-02952-2	Sequence 2, Appli
6	437.5	25.6	356	15	US-09-125-619-2	Sequence 2, Appli
7	437.5	25.6	356	15	US-09-125-619-13	Sequence 13, Appl
8	417.5	24.4	208	15	US-09-125-619-47	Sequence 47, Appl
9	416	24.4	211	15	5 US-09-125-619-37	Sequence 37, Appl

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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⊢	24	24	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	<u>1</u> 5	15	15	15	15
α	-60-191-681-16	-60-191-637-206	-09-125-619-3	-09-125-619-1	-09-125-619-2	-09-125-619-1	-09-125-619-2	-09-125-619-2	-09-125-619-1	-09-125-619-2	US-09-125-619-24	-09-125-619-2	-09-125-619-2	-09-125-619-2	9-125-619-1	-09-125-619-1	-09-125-619-4	-09-125-619-1	-09-125-619-2	-09-125-619-4	-09-125-619-2	-09-125-619-3	9-125-619-4	-09-125-619-4	9-125-619-4	-09-125-619-4	-09-125-619-4	-09-125-619-3	-09-125-619-3	-09-125-619-3	5-619-3	-09-125-619-3	-09-125-619-4	-619-3
4	16	20	30	"	10		•••				Sequence 24			10	w	æ	w	Sequence 15	w	w					Sequence 46							Ø	Sequence 43	Sequence 31
Appli	220,	, 009	, App	1, Appl	-	•	•	7, Appl	•	`	`	•	•	•	•	•	L, Appl	•	•	•	•	•	•	•	-	•), Appl	•	•	•	5, Appl	•	•	L, Appl

ALIGNMENTS

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RESULT 1
US-09-445-803-2
US-09-445-803-2
Sequence 2, Application US/09445803
GENERAL INFORMATION: Adminis. of Tulane Educational, Fund
Philipp, Mario T.
TITLE OF INVENTION: Surface Antigens and Proteins Useful in
Compositions for the Diagnosis and Prevention of Lyme
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Howson and Howson
STREET: Spring House Corporate Cntr., P.O. Box 457
CITY: Spring House Corporate Cntr., P.O. Box 457
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/445,803
FILING DATE: 30-JUN-1997
AFTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 60/051,271
FILING DATE: 30-JUN-1997
AFTORNEY/AGENT INFORMATION:
NAME: Bak, MATY E.
REGISTRATION NUMBER: 31,215
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PPLICANT: Philipp, Mario T.

PPLICANT: Liang, Fang Ting

FITTLE OF INVENTION: Novel Peptides and Assays for

FILE REFERENCE: TUL3USA

CURRENT FILING DATE: 1999 04-28

NUMBER OF SEQ ID NOS: 11

SOOTWARE: Patentin version 3.1

SEQ ID NO 9

LENGTH: 349

TYPE: PRT

ORGANISM: Borrelia garinii
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Best Local S
Matches 348
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Best Local Similarity
Matches 349; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
AKGIKGIVDAAGKADAKEGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVA 120
                                                    AVDIIKAAAEAASAASAATGSAAIGDVVNGNGATAKGGDAKSVNGIAKG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTNPIDAAIGGAGDNDAAAAFATMKKDDQIAAAMVLRGMAKDGQFALKDAAAAHEGTVKN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTNADAGKLFYKNAGNYGGEAGDAGKAAAAVAAYSGEQILKAIYHAAKDGGEKQGKKAAD 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKGIKGIVDAAGKADAKEGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKGIKGIVDAAGKADAKEGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: TUL2APCT
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                                                                                                                  Conservative
                                                                                                                            99.6%;
99.7%;
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                                                                                                                            Score 1702; DB 17;
Pred. No. 3.2e-136;
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Pred. No. 9.7e-137;
; Mismatches 0;
                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                             for the Diagnosis of Lyme Disease
                                                                                                                                          Length 349;
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US-09-300-971A-11
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GENERAL INFORMATION:
APPLICANT: Philipp, Mario T.
APPLICANT: Liang, Fang Ting
TITLE OF INVENTION: Novel Peptides and Assays for the Diagnosis of Lyme Disease
                                                                               Sequence 10, Application US/09300971A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENCTH: 323
TYPE: PRT
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Best Local Similarity
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APPLICANT: Liang, Fang Ting
TITLE OF INVENTION: Novel Peptides and Ashays
FILE REFERENCE: TUL3USA
CURRENT APPLICATION NUMBER: US/09/300,971A
CURRENT FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 11
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                                                                                                                                                                                                  AAAEAASAATGSAATGDVVNGNGATAKGGDAKSVNGIAKG
                                                                                                                                                                                                                                                        I---GDRDGDAEFNQDGMKKDDQIAAAIALRGMAKIJGKFAVKDGGEKAEGAIKGVSELLD
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                                                                                                                                                                                                                                                                                              IGGAGDNDAAAAFAT--MKKDDQIAAAMVLRGMAK)GQFAIKDAAAAHEGTVKNAVDIIK 306
                                                                                                                                                                                                                                                                                                                                  LEGKAGANAHGDSEAASKAAGAVSAVSGEQILSAIVKAAGEAGDQEGKKPEEAKNPIAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDQIAAAIALRGMAKDGKFAVKK--DEKGKAEGAIKGASELLDKLVKAVKTAEGASSGTA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTNVNA-----GKLFVKRAADDGGDADDAGKAAAAV-----AASAATGNA 128
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42.9%; Pred. No. 9.5e-37;
vative 42; Mismatches 110;
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PATHOGENIC BORRELIA

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; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-09-300-971A-10
    Вb
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PCT-US97-02952-2
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                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Best Local
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CURRENT FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: TUL3USA
                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acids
TOPOLOGY: line-
WOLECUTE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 KQG-KKAADRTNPIDAAIGGAGDNDAAAAFATMKKDDQIAAAMVLRGMAKDGQFALKD 289
::| :||:||:||:||:||:||
118 EKGVADVKEATNPIEAAIGSTGDNDAAAFQDEMKKNDQIAAAIVLRGMAKDGEFALKD 175
                                                                                                                                                                            139 AKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNA-AGAEGTTNADAGKLEVKNAGNV 197
                                                                                                                                                                                                                               103 GKPDSTGSVGTA-----VEGAIKEVSELLDKLVKAVKTAEGASSGTAAIGEVV-ADA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 LNAAGAEGTTNADAGKLEVKNAGNVGGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDGGE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AAVAASAATGN-AAIGDVV---NGDVAKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGK 172
                                                                                                                                                      154 DAAKVADKASVKGIAKGIKEIVEAAGGSE----KLKAVAAAKGENNKGAGKLFGKAGAAA 209
266 GAEFGQDEMKKDDQIAAAIALRGMAKDGKFAVKD-----GEKEKAEGAIKGAAESAVRK 319
                                    258 AAAFA--TMKKDDQIAAAMVLRGMAKDGQFALKDAAAAHEGTVKNAVDIIKAAAEAA--S 313
                                                                                                                                                                                                                                                                          79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                               GGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPIDAAIGGAGDNDA 257
                                                                                                                                                                                                                                                      GKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDV 138
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                                                                                                                                                                                                                                                                                                             127;
                                                                           HGDSEAASKAAGAVSAVSGEQILSAIVTAA-DAAEQDGKKPEEAKNPIAAAI---GDKDG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEAAAGDGNKDACAGKLFAKNAANGGGGAAAAEKAAAAVSAVSGKQILKAIVDAA--GKE 117
                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                               25.6%; Score 437.5; DB 1 46.9%; Pred. No. 1.2e-28;
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                                                                                                                                                                                                                                                                                                             26; Mismatches
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Pred. No. 1.2e-32;
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SEQ ID NO 2
LENGTH: 356
TYPE: PRT
ORGANISM: Borrelia burgdorferi
              FILE REFERENCE: UTSH:234
CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 356
                                                                                                                                                                                                                                                                                      Sequence 13, Application US/09125619 GENERAL INFORMATION:
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Best Local Similarity
Matches 127; Conserv
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                  APPLICANT: BARBOUR, ALAN G.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                                    APPLICANT: NORRIS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF
FILE REFERENCE: UTSH:234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 GGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPIDAAIGGAGDNDA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 GKPDSTGSVGTA------VEGAIKEVSELLDKLVKAVKTAEGASSGTAAIGEVV-ADA 153
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HARDHAM, JOHN M.
HOWELL, JERRILYN K.
BARBOUR, ALAN G.
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HARDHAM, JOHN M.
HOWELL, JERRILYN K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.6%; Score 437.5; DB 15; 46.9%; Pred. No. 1.2e-28;
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87;

Indels Length 356;

31;

Gaps

11;

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Sequence 47, Application US/09125619
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: BARBOUR, ALAN G.
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US-09-125-619-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 47
LENGTH: 208
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.6%; Score 437.5; DB 15; Length 356; Best Local Similarity 46.9%; Pred. No. 1.2e-28; Matches 127; Conservative 26; Mismatches 87; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH: 234
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
PRGANISM: Borrelia burgdorferi
09-125-619-47
                                                                                                                                                              198 GGEAGDĀGKAAĀAVĀAVSGEQILKAIVHĀAKDGGEKQGKKĀADRTNPIDAAIGGAGDNDA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 AKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNA-AGAEGTTNADAGKLFVKNAGNV 197
                                                                                                                             199
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168 GDG---MKKDDQIAAAIALRGMAKDGKFAVKNDEKGKAEGAIK 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 VLGAITG--LIGDAVS-SGLRKVGDSVKAAS 347
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                                                                                                                                                                                                                                                                                          79 GKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDV 138
                                                                                                                                                                                                                                                       4
                   AAAFATMKKDDQIAAAMVLRGMAKDGQFALK-DAAAAHEGTVK 299
                                                                                                   GEAGDAGKAAAAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPIDAAIG-GAGDNDA 257
                                                                                                                                                                                                                                                   GKPDSTGSVGTA-----VEGAIKEVSELLDKLVTAVKTAEGASSGTDAIGEVVDND- 54
                                                                            110; Conservative
                                                                                                                                                                                                                                                                                                                                 24.4%; Score 417.5; DB 15; Length 208;
49.3%; Pred. No. 2.9e-27;
ative 24; Mismatches 68; Indels 21; Gaps
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RESULT 10
US-09-125-619-34
; Sequence 34, Application US/09125619
; GENERAL INFORMATION:
; GENERAL INFORMATION:
                                                                                                                  SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34
LENGTH: 214
TYPE: PRT
ORGANISM: Borrella burgdorferi
US-09-125-619-34
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GENERAL INFORMATION:
APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HARBOUR, ALAN G.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE DEF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
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; ORGANISM: Borrelia burgdorferi
US-09-125-619-37
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US-09-125-619-37
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CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 37
LENGTH: 211
                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 24.4%; Score 416; DB 15; Best Local Similarity 49.1%; Pred. No. 3.9e-27; Matches 109; Conservative 26; Mismatches 71;
    Matches 110;
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: BARBOUR, ALAN G.
                                                                                                                                                                                                                                                   APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234
CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
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  Conservative
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24.2%; Score 412.5; DB 15;
48.9%; Pred. No. 7.9e-27;
7ative 24; Mismatches 72;
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19;
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79 GKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDV 138

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AKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNAAGAEGTTNADAGKLFVKNAGNVG 198 GKPDSTGSVGTA-----VEGAIKEVSELLDKLVKAVKTAEGASSGTAAIGEVVDND-

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US-09-125-619-43
(US-09-125-619-43)
(Sequence 43, Application US/09125619)
(GENERAL INFORMATION:
APPLICANT: APPLICANT: STEVEN J.
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SEQ ID NO 31
LENGTH: 212
TYPE: PRT
ORGANISM: Borrella burgdorferi
US-09-125-619-31
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US-09-125-619-31
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Best Local Similarity
Matches 112; Conserv
APPLICANT: JING-RÈN, ZHANG
APPLICANT: HARDEAM, JOHN M.
APPLICANT: HOWELL, JERRILIN K.
APPLICANT: HOWELL, JERRILIN K.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC FILE REFERENCE: UTSH:234
CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
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CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
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TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH: 234
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HARDHAM, JOHN M.
HOWELL, JERRILYN K.
BARBOUR, ALAN G.
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49.8%; Pred. No. 1.4e-26;
ative 21; Mismatches 71; Indels 21;
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US-09-125-619-38
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TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234

CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 38, Application US/09125619
GENERAL INFORMATION:
APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILLYN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ve
SEQ ID NO 43
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Matches
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Best Local Similarity
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TYPE: PRT
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  168
                                        254 DNDAAAAFATMKKDDQIAAAMVLRGMAKDGQFALKDAAAAH--EGTVK 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 GGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPIDAAIGGAGDNDA 257
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                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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ADDGAEFGDGMKKDDQIAAAIALRGMAKDGKFAVKSGGEKEKAEGAIK 215
                                                                                                      GNVGGEAGDAGKAAAAVAAVSGEQIIKAIVHAAKD-GGEKQGKKAADRTNPIDAAIGGAG 253
                                                                                                                                                                                   AKAKGGDAASVNGIAKGIKGIVDAA---EKADAKEGKLNAAGAEGTTNADAGKLFVK-NA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAAKVADKASVKGIAKGIKEIVEAAGGSE----KLKAVAAAKGENNKGAGKLFGKAGAAA 110
                                                                               GN-AGDSEAASKAAGAVSAVSGEQILSAIVKAAGEAAGDQEGKKPGEAKNPIAAAIGKGN 167
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                                                                                                                                                                                                                                                                                                                                               24.0%; Score 409.5; DB 1 48.7%; Pred. No. 1.4e-26;
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US-09-125-619-36

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Sequence 36, Application US/09125619
GENERAL INFORMATION:
APPLICANT: NORRIS, STEVEN J.
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HARDHAM, JOHN M.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH: 234
CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 36
LENGTH: 215
TYPE: PATENTIAN BOITELIA burgdorferi
US-09-125-619-36
                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/125,619
; CURRENT FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 35
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-09-125-619-35
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                                       Query Match 23.7%; Score 405.5; DB 15; Length 214; Best Local Similarity 49.1%; Pred. No. 3.1e-26; Matches 112; Conservative 21; Mismatches 70; Indels 25;
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Best Local S
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TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: BARBOUR, ALAN G.
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Neral INFORMATION: CTEVEN J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 AAAF-ATMKKDDQIAAAMVLRGMAKDGQFALKDAAAAH---EGTVK 299
79 GKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 A-AKAADKESVIGIAKGIKEIVEAARGSE----KLKAVAAAKEGNEKAGKLEGK-AGAAA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 GKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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49.1%; Pred. No. 1.9e-26;
ative 22; Mismatches 73;
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Search completed: January 10, 2002, 14:08:25 Job time: 359 sec

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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US00_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US00_NEW_COMB.pep:*
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12.: y 27.: y 27.: TGNAAIGI : : : LSTAQVA. NVNAGKLI :: : DLNKIKSI GIAKGIK	Application US/099 RMATION: Glenn, Matthew Havukkala, Ilkka Bloksberg, Leonard Lubbers, Mark Dekker, James Christensson, Anna Holland, Ross O'Toole, Paul Reid, Julian COolbear, Timothy TVENTION: Lactobacil VENTION: Lactobacil Reid, Julian COOLBER: US TICATION NUMBER: US LICATION NUMBER: US LICATION NUMBER: US LING DATE: 2001-10-08-08 GD DATE: 2000-11-28 GD DATE: 2000-11-28 GD DATE: 2000-11-08-08 GD DATE: 2000-11-08-08 GD DATE: 2001-08-08 GD DATE: 2001-08-08 GD DATE: 2000-11-08-08 GD DATE: 2000-11-08-08 GD DATE: 2000-11-08-08 GD DATE: 2001-08-08 GD DATE: 2001-0		892 2478 7330 75281 1502 480 488 488 488 488 488 5792 885 5793
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tch 12.9%; Score 220; DB 5; Length 1463; al Similarity 27.1%; Pred. No. 2.8e-05; g2; Conservative 41; Mismatches 145; Indels 62; G AAEEAASAASAATGNAAIGDVVKNSGAAAKGGEAASVNGIAKGIKGIVDAAGKADAKEGK	71536 lus rhamnosus n 709/971,536 92 NO. 09/634,23 NO. 09/724,63 NZ01/00160 Version 4.0	ALIGNMENTS	US-09-952-267A-5 US-09-815-242-5816 US-09-815-242-12967 US-09-708-427-1373 US-09-815-242-12996 US-09-897-516-7005 US-09-897-516-7005 US-09-620-394B-2384 US-09-708-427-11369 US-09-620-394B-2383 US-09-620-394B-2383 US-09-620-394B-2383 US-09-620-394B-2383 US-09-620-394B-2383 US-09-620-394B-2383 US-09-620-394B-2383 US-09-620-394B-2383 US-09-620-394B-2383 US-09-857-128-13 US-09-815-242-5635 US-09-815-242-5635 US-09-815-242-12389 US-09-815-242-12389 US-09-815-242-12389
Length 1463; i5; Indels 62; G akgIkgIvDaAgkADAKEGK	Polynucleotides,	<i>;</i>	
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Gaps GK 80 : KQ 892 DV 138 DV 138 SY 950	Polypeptides		5, Appli 5816, Ap 12967, A 1373, Ap 12996, A 7005, Ap 11370, Ap 11369, A 2384, Ap 11368, A 2383, Ap 11368, A 2383, Ap 11368, A 2383, Ap 11368, A 2383, Ap 11368, A 2383, Ap 1283, Ap
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951 AHQAGSSAS------DAV-----GQSGSAAQHASTAASAASSYPKDSGIQS 990

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PLICANT: PHILIPPE, Michel
PLICANT: GARSON, Jean-Claude
PLICANT: GARSON, Jean-Claude
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: LASST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: LASST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
CURRENT APPLICATION NUMBER: US/09/861,597
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 09/247,806
PRIOR FILING DATE: 1999-02-11
PRIOR FILING DATE: 1998-02-11
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Best Local Similarity
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AGRGGQGAGAAAAAAGGAGQG 600
                                                                                 GAGRGGLGGQGAGAAAAAAAAGGAGQGGLG-SQGAGQGAGAAAAAAGGAGQGGYGGLGSQG
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                                        NGNGATAKGGDAKSVNGTAKG 349
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; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                             Sequence 1, Application US/09861597 GENERAL INFORMATION:
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Best Local Similarity 26.5%;
Matches 101; Conservative 3
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 8
LENGTH: 606
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APPLICANT: ARRAUDEAU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERNATOLOGICAL COMPOSITION CONTACTING
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR A
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6388-0365-0
CURRENT APPLICATION NUMBER: US/09/861,597
CURRENT FILING DATE: 2001-05-22
CURRENT FILING DATE: 2001-05-22
                                                                       APPLICANT: PHILLIPPE, Michel
APPLICANT: GARSON, Jean-Claude
APPLICANT: GARSON, Jean-Claude
APPLICANT: ARRAUDEAU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR A
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6388-0365-0
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PRIOR APPLICATION NUMBER: 09/247,806
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: FR 98/01614
PRIOR FILING DATE: 1998-02-11
                        CURRENT APPLICATION NUMBER: US/09/861,597
CURRENT FILING DATE: 2001-05-22
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PRIOR APPLICATION NUMBER: 09/247,806
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; SOFTWARE: PatentIn Ver. 2.1
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; TYPE: PRT
; ORGANISM: Nephila clavipes
US-09-861-597-1
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NERAL INFORMATION:
PLICANT: PHILLIPPE, Michel
APPLICANT: GARSON, Jean-Claude
APPLICANT: ARRAUDEAU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6388-0365-0
COURSELVE AND LOCAL COSMETIC OR ANALOG
FILE REFERENCE: 6388-0365-0
                                                                                                                                                                 PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: FR 98/01614
PRIOR FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
Query Match
Best Local Similarity
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Best Local
                                                                                    LENGTH: 606
TYPE: PRT
ORGANISM: Nephila clavipes
-09-861-597-4
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CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 09/247,806
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PRIOR APPLICATION NUMBER: FR 98/01614
PRIOR FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 14
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11.4%;
26.4%;
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Score 194.5; DB 5; Pred. No. 0.00031;
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                 Length 606;
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CURRENT APPLICATION NUMBER: US/09/971,536
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: U.S. NO. 09/634,238
PRIOR FILING DATE: 2000-08-08
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: PCT/NZ01/00160
PRIOR FILING DATE: 2001-08-08
                                                                                                                                                                                                         SEQ ID NO 70
LENGTH: 1879
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                                                                        Matches
                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 70,
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                                                                                                                                                                                                                                                SOFTWARE: FastSEQ
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                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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1252 DHDATLTANEKASQKQAVTDEATKAKKAIDAAKQADAVDQAKTDGIKAIDAQHHSGQALD 1311
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                                                                      Local Similarity 26. nes 110; Conservative
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                        4 DHD-----NHKGTVKNAV-DMAKAAEEAASAASAATG-NAAIGDVVKNSGAAAKGGEAAS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGGYGGLGSQGAGRGGLGGQGAGAAAAAAAGGA-GQGGLGSQGAGQGA----GAAAAAAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Christensson,
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Bloksberg, Leonard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dekker, James
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                                                                                      10.7%;
26.6%;
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                                                                      Score 182; DB 5;
Pred. No. 0.0049;
5; Mismatches 154
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                                                                        154;
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                                                                                                   Length 1879;
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                                                                        Indels 114;
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                                                                      Gaps
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US-09-500-746-17
Sequence 17, Application US/09500746
GENERAL INFORMATION:
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SEQ ID NO 17
LENGTH: 410
TYPE: PRT
ORGANISM: Human
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APPLICANT: Seki, Tetsunori
TITLE OF INVENTION: USES OF INHIBITORS FOR THE ACTIVATION OF CXCR4 RECEPTOR BY SDF-1
TITLE OF INVENTION: TREATING RHEVMATOID ARTHRITIS
FILE REFERENCE: 0575/57005-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/500,746
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1566 GEVAKITDAIDHDPTLTDAEKATQKQAVIAEADKAKKAIDAAGDADAVDQAQK 1618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1456 TAGIKAIDEQHKSGQTVDARKEDAKKAIDAEAG-KVTDAIDHDATLTAAQKEAQKQAVAD 1514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 GTVKNAVDIIKAAAEAASAASAATGSAAIGDVVNGNGATAKGGDAKSVNGIAK 348
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      327
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                                        268 DQIAAAMVLRGMAKDGQFALKDAAAAHEGTVKNAVDIIKAAAEAASAASAATGSAAIGDV 327
                                                                                       279
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                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 10.1%; Score 172.5; DB 5; Length 410; Local Similarity 27.5%; Pred. No. 0.0036; nes 102; Conservative 11; Mismatches 161; Indels 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57
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                                                                                GCAACAGCCAAAGAGG-----ACTTNCCGCTAGACCCACTCGAGGAAAACTAA---- 326
                                                                                                                         GEQILKAIVHAAKDGGEKQGKKAADRTNPIDAAIG------GAGDNDAAAAFATMKKD 267
                                                                                                                                                                 CCCGAAGCNANAGTGGATNCAGGAGTACCTGG-----AGNNAACTATGAACAANTAAGC 278
                                                                                                                                                                                                                                               KRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDVAKAKGGDAASVNGIAKGIKGI 159
                                                                                                                                                                                                                                                                                                                                AAGAAGGCNACGTCAANAAGGACGAATATTTGCAANGNNGNNCAGGGCTGTNCNCG---- 173
                                                                                                                                                                                                                                                                                                                                                                                                               NGGNNNAGANANTGNNTGGAGAANGACAANGGGGGNGTCGNNGGAGCNGNTGTGAGTGGG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NDHDNHKGTVKNAVDMAKAAEEAASAASAATGNAAIGDVVKNSGAAAKG--GEAASVNGI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GEAGDAGK--AAAAVAAVSGEQILKAIVH-AAKDGGEKQGKK--AAD 240
                                                                                                                                                                                                                                                                                                                                                                           AKGIKGIVDAAG--KADAKEGKLDATGAEGT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -DAKEG-----KLNAAGAEG-----TTNADAGKLFVKNAGNV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -KADAKQ-VIDAEAAKVTAAIDQDNTLTKAQKAAQKQGVATEADK 1356
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    -AACCTTGT-----GAGAGATGAAAGGNCAAAGAC 355
                                                                                                                                                                                                                                                                                                                                                                      -----TNVNAGKLEV 99
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                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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US-09-249-585A-3
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                                                                                                                                                                                                                                             Sequence 616, Application US/09976594
Sequence 616, Application US/09976594
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROI
FILE REFERENCE: PA-0041 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.0 SEQ ID NO 3 LENGTH: 641
                                                                              SOFTWARE: PERL Program
SEQ ID NO 616
LENGTH: 605
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APPLICANT: Horlick, Robert
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Best Local
                                                                                                                                                      CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/976,594 CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
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                                                                                                                                              NUMBER OF SEQ ID NOS: 1143
                                    ORGANISM: Homo sapiens
                                                             TYPE: PRT
                     FEATURE
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 ASVNGIAKGIKGIVDAAEKADAKEGKLNAAGAEGITNADAGKLFVKNAGNVGGEAGDAGK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 85; Conserv
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US-09-952-267-7
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                                                                                                                                                                                                                                                   ; LENGTH: 624
TYPE: PRT
; ORGANISM: MOTAXELLA CATARTHALIS
US-09-952-267-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: unknown or other US-09-976-594-616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09952267 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 7
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Best Local
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APPLICANT: AEBI, CHRISTOF
APPLICANT: COPE, LESLIE [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
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                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 98
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NAME/KEY: unsure
LOCATION: 596
                                                                                                                                                                                                                                                                                                                                                                                     COR APPLICATION NUMBER: 09/336,447 RIOR FILING DATE: 1999-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                              URRENT APPLICATION NUMBER: US/09/952,267 RRENT FILING DATE: 2001-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 TNPIDAAIGG-----AGDNDAAAAFATMKKDDQIAAAMVLRGMAKDGQFALKDAAAAHEG 296
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les 103; Conserv
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VGGGFDNRATGNYSVISGGFDNQAKGEHSTI---
                                  IKGIVD--AAGKADAKEGKLD--ATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTTTACAGACCCACCGGTTAAGA------CAAAATTTGGATATCATATTATTGG 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCAGGCAAGGGGGTGACTTG--GGTTGGATGACCAGAGGGTCCATGGTGGGACCATTTC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDVVNGDVAKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNAAGAEG-----TTNA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTCTGG----GATGAGATTCAATG-----AAGTGGCCGCACAGTATAGTGAAGATAAA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGKADAKEGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAI 130
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                                                                                                           KGTVKNAV---DMAKAAEEAASAASAATG--NAAIGDVVKNSGAAAKGGEAASVNGIAKG 63
                                                                         KGHTKKAVLGSLLIVGALGMATTASAQTGSTNAANGNIISGVGAYVGGGVINQAKGNYPT 82
                                                                                                                                                      ; 68
                                                                                                                                                                      Similarity
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COPE, LESLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MACIVER, ISOBEL
FISKE, MICHAEL J.
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                                                                                                                                                  %; Score 167.5; DB 5; Length
%; Pred. No. 0.01;
42; Mismatches 145; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5; Length 605
--- AGGESNQATGRNSTV 128
                                                                                                                                                                                      Length 624;
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US-09-952-267A-7
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Best Local :
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APPLICANT:
APPLICANT:
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APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS
FILE REFERENCE: AMCY:024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HANSEN, ERIC J. APPLICANT: AEBI, CHRISTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/09/336,447A PRIOR FILING DATE: 1999-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/952,267A CURRENT FILING DATE: 2001-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 624
TYPE: PRT
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297 YDIEINQDNIKDLQKEVKGLDKEVGVLSRDIGSLHDDVADNQADIAKNKAD 347
                                           270 IAAAM-----
                                                                                    245 VSKADNGTVSVGSQGKERQIVHVGAGQISDDSTD----AVNGS----QLYALATAVDDNQ
                                                                                                                             219 ILKA---IVHAAKDGGEKQ------GKKAADRTNPIDAAIGGAGDNDAAAAFATMKKDDQ 269
                                                                                                                                                                        185 AAIGSENTVNENQKNVFILGSNTTNAQSGSVLLGHETSGKEATAVSRARVNGLTLKNFSG
                                                                                                                                                                                                                  175 AA-GAEGTTNADAGKLFVKNAGNVGGEAGD-----AGKAAAAV--AAVSG-----EQ
                                                                                                                                                                                                                                                             129 A--GGSNNQAVG--TNSTVAGGSNNQAKGANSFAAGVGNQANTDNAVALGKNNTINGNNS 184
                                                                                                                                                                                                                                                                                                        120
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                                                                                                                                                                                                                                                                                                                                                                                          64 IKGIVD--AAGKADAKEGKLD--ATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                      23 KGHTKKAVLGSLLIVGALGMATTASAQTGSTNAANGNIISGVGAYVGGGVINQAKGNYPT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 KGTVKNAV---DMAKAAEEAASAASAATG--NAAIGDVVKNSGAAAKGGEAASVNGIAKG
                                                                                                                                                                                                                                                                                                                                                    VGGGFDNRATGNYSVISGGFDNQAKGEHSTI-------AGGESNQATGRNSTV 128
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                                                                                                                                                                                                                                                                                                    AASAATGNAAIGDVVNGDVAKAKGGDAASVNGIAKGIKGIVD-----AAEKADAKEGKLN 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89;
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COPE, LESLIE D.
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                                      ----VLRGMAKDGQFALKDAAAAHEGTVKNAVDIIKAAAE 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%; Score 167.5; D 25.4%; Pred. No. 0.01;
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RESULT 12 PCT-US01-20545-4

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PLICANT: PHILLIPPE, Michel
PPLICANT: GARSON, Jean-Claude
APPLICANT: ARRAUDEAU, Jean-Pierre
APPLICANT: ARRAUDEAU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERNATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6388-0365-0
CURRENT APPLICATION NUMBER: US/09/861,597
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 09/247,806
PRIOR APPLICATION NUMBER: FR 98/01614
PRIOR FILING DATE: 1999-02-11
PRIOR FILING DATE: 1998-02-11
UNMBER OF SEQ ID NOS: 14
COMMENDE: NOTATION OF SEQ ID NOS: 14
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; LENGTH: 588
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
PCT-US01-20545-4
                                                                                                                     ; TYPE: PRT ; ORGANISM: Nephila clavipes US-09-861-597-2
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US-09-861-597-2
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SEQ ID NO 2
LENGTH: 529
  Query Match
Best Local Similarity
Matches 96; Conserv
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TITLE OF INVENTION: MYCOBACTERIAL PROTEINS AS EARLY ANTIGENS FOR SERODIAGNOSIS
FILE REFERENCE: 32004-173355
CURRENT APPLICATION NUMBER: PCT/US01/20545
CURRENT FILING DATE: 2001-06-17
PRIOR APPLICATION NUMBER: US 60/212,048
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VDAAEKADAKEGK---LNAAGAEGTTNADAGKLFVKNAGNVGGEAGDAGKAAAAVAAVSG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDADDAGKAA----AAVAASAATGNAA---IGDVVNGDVAKAKGGDAASVNGIAKGIKGI 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDGGNGGTGGTGGRGGDGGSGGAGGASGWLMGNGGNGGNGGTGGSGGVGGNG---GIGG- 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -DGAGGGNATSTSSIPFDAHGGNGGAGGDAGH-----GGTGGDGGDGGH-----AGTGG 517
       Conservative
9.3%; Score 158.5; DB 5; 25.6%; Pred. No. 0.028; tive 21; Mismatches 171;
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US-09-995-493-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 100; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hillman, Jeffrey
APPLICANT: Progulske-Fox, Ann
TITLE OF INVENTION: Identification of Actinobacillus actinomycetemcomitans Antigen
TITLE OF INVENTION: in the Diagnosis, Treatment, and Monitoring of Periodontal Di
FILE REFERENCE: MBHB01-662
CURRENT APPLICATION NUMBER: US/09/995,493
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 234
SOFTWARE: Patentin version 3.0
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APPLICANT: Hillman, Jeffrey
APPLICANT: Progulske-Fox, A
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                                             147
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                                                                                                                                                                                                                                                                                                                                                                      493 DSNYDN-KG-----AKAVGSIALGEKATTGTAMMSIAIGLNSNVSGQNTVALGANI 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167
                                                                                           664 LLAGKNLAVKQNGTNFTFSTQENVTFTNVTTQDLTATGNTTVKNFSVQNGGTINMGNN-- 721
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                                                                                                                                                                                    KNVAAGNVAANSTDAVNGSQLFAVASRVEQGWQITSGVENGGTQNGAASTATIKPSNQVK 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQGPGGYGPGQQGPGGYGPGSASAAAAAAAGPGQQGPGGY---GPGQQGPSGPGSASAA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTVKNAVDIIKAAAEAA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAASAAASAESGGPGGYGPG----QQGPGGYGPGQQGPGGYGPGQQG-PSGPGSAAAAA 166
                                        ASVNGIAKG-----IKGIVDAAEKADAKEGKLNAAGAEGTTNADAGKLFVKNAG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----AAAAAAGPGGYGPGQQGPGGYAPCQQGPSGPGSASAAAAAAAAAAGPGGYG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKAADRTNPIDAAIGGAGDNDAAAAFATMKKDDQTAAAMVLRGMAKDGQFALKDAAAAHE 295
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-RITGVAEGTQDDDAVNEKQLKSLLGGSASTEIVEKKAAQAGDENL--ADISVANGKNAG
                                                                                                                                                                                                                               KLDATG---AEGTTNVNAGKLF------VKKAADDGGDADDAGKAAAAVAAS--- 122
                                                                                                                                                                                                                                                                                                                        -----GDVVKNSGAAAKGG-----EAASVNGIA-KGIKGIVDAAG------KADAKEG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.2%; score 157.5; DB 5; llarity 20.7%; Pred. No. 0.095; Conservative 53; Mismatches 157;
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FILE REFERENCE: SCH-1763
CURRENT APPLICATION NUMBER: US/09/646,673A
CURRENT FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: PCT/DE99/00908
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 202
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 172
LENGTH: 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HINZMANN, BERND
APPLICANT: SCHMITT, ARMIN
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: DAHL, EDGAR
APPLICANT: ROSENTHAL, ANDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ROSENTHAL, ANDRE
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
TITLE OF INVENTION: TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SPECHT, THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2-646-673A-172
Lence 172, Application US/09646673A
ERAL INFORMATION:
                            276 LRGMAKDGQFALKDAAAAHEGTVKNAVDIIKAAAEAASAASAATGSAA 323
  338 APSAAGPGAPPEQEAAPAEE-----
                                                                                                                                                                                                                              167 DAKE-GKLNAAGAEGTTNADAGKLFVKNAGNVGGEAGDAGKAAAAVAAVSGEQILKAIVH 225
                                                                                                                                                                                                                                                                                               174 GSATAAEGEAASAASSTSSPKAEDGATPSPSNETPKKKKKRFSFKKSFKLSGFSFKKNKK 233
                                                                                                                                                                                                                                                                                                                                             119 VAASAATGNAAIGDVVNGDVAKAKGGDAASVNGIAK-----GIKGIVDAAEKA 166
                                                                                                                                                                                                                                                                                                                                                                                               120 -----SAPAADKEEPAAAGSGAASPSSAEKGEPAAAAAPEAGASPVEKEAPAEGEAAEP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          945 NGD 947
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                                                                                                                                              226 AAKDGGEKQGKKAADRTNPIDAAIG----GAGDNDAAA---AFATMKKDDQI---AAAMV 275
                                                                                                                                                                                            234 EAGEGGEAEAPAAEG-----GK--DEAAGGAAAAAAEAGAASGEQAAAPGEEAAAGEEG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 GGD 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 NVGGE-----AGDAGKAAAAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPID 246
                                                                                                                                                                                                                                                                                                                                                                                                                                             64 IKGIVDAAGKADAKEGKLDATGAEGTTNVNAGKLFVKRAADDGG-----DADDAGKAAAA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 KTAAKGEAAAERPGEAAVASSPSKANGQENGHVKVNGDASPAAAESGAKEELQANG---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 KNAVDMAKAAE---EAASAASAATGNAAIGDVVKNSG----AAAKGG--EAASVNGIAKG 63
                                                                                               AA--GGDPQEAK-----PQEAAVAPEKPPASDETKAAEEPSKVEEKKAEEAGASAAACE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PAAAAASSACAAPSQEA 374
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Search completed: January 10, 2002, 14:08:51 Job time: 320 sec

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Result
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               number of hits satisfying chosen parameters:
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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RESULT T31328

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C; Species: Antheraea pernyi (Chinese oak silkmoth)

fibroin - Chinese oak silkmoth

Qу Db	Оу	Db Qy	Qу	Qγ	Фр	Qu Be Ma	RESULT 140300 outer r C; Spec. C; Date C; Acces R; Rest. Mol. M A; Titl A; Refe; A; Statt A; Ressi A; Cross C; Genei A; Genei		
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						Query Match Best Local Similarity Matches 114; Conser	RESULT 1 140300 outer membrane lipoprotein - Bc C;Species: Borrelia hermsii C;Date: 12-Aug-1996 #sequence_r C;Accession: 140300 R;Restrepo, B.I.; Kitten, T.; C Mol. Microbiol. 6, 329-3311, 1 A;Title: Subtelomeric expressic A;Reference number: 140300; MUI A;Accession: 140300 A;Status: preliminary; translat A;Molecule type: DNA A;Residues: 1-353 <res> A;Cross-references: GB:L04788; C;Genetics: A;Gene: vmp17</res>		184.5 183.5 182 182 181.5 181.5 180.5 179.5 179.5 179.5 179.5 179.5 179.5 179.5 179.5 179.5 179.5 179.5 179.5 179.5 179.5 179.5
KAAAEAASAASAATGSAAIGDVV- : : : NSAAASAVNKILSTLIIAIRNTVD	GAGDNDAA PAKDNKKEIKDGA	GGEAGDAGKAAAAVAAVSGEQILKAIVHA : :: : : : RADNAAAQAAAASIGAVTGADILQAIVQS	AKGGDAASVNGIAKGIKGIVDAA : : AVPGEATSVNSLVKGIKEIVGVV	KLQDEVA	NSGAAAKGGEAASVNGIAKGIKGIVD- :	ilarity Conser	ipoproti 196 #se 196 #se 300 300 300 meric e er: 140 300 inary; DNA DNA DNA CB:		10.7 10.7 10.7 10.6 10.6 10.6 10.5 10.5 10.5 10.5 10.5
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NGNGATAKGGDAKSV 	AAA	VAKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNAAGAEGTINADAGKLFVKNAGNV	MTSVKKKLQDEVAKNGNYPKVKTAVDEFVAILGKIEKGÅKBASKGÅTGVIIGNTINTINTINTINTINTINTINTINTINTINTINTINTIN	NAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVV-NGD	NSGAAAKGGEAASVNGIAKGIKGIVDAAG-KADAKEGKLDATGAEGT 	Score 266.5; DB 2; Le Pred. No. 1.8e-07; 36; Mismatches 122; In	elia hermsii ision 12-Aug-1996 #text_ ter, C.J.; Infante, D.; 2 regions of Borrelia herm 93133110 from GB/EMBL/DDBJ	ALIGNMENTS	H70589 F70824 F70963 T31110 JV0057 F70580 G70917 EART S33441 EAMS T08509 C70720 A70896 BP0523 A48658
343 336			DAGKLFVKNAGNV 197 DIGKLFTATTDAN 192	GNAAIGDVV-NGD 137 : : GDVIIGNTVKNGD 139	GKLDATGAEGT 89 :	Length 353; Indels 73; Gaps 15;	hange 08-Oct-1999 arbour, A.G. ii linear plasmids are 1; PID:g144024		hypothetical glyci hypothetical glyci hypothetical glyci extracellular matr tolA protein - Esc hypothetical glyci hypothetical glyci hypothetical glyci elastin precursor EF protein - Strep elastin precursor trbL protein - Ent hypothetical glyci hypothetical glyci hypothetical glyci hypothetical glyci hypothetical glyci hypothetical glyci hypothetical glyci hypothetical glyci hypothetical glyci hypothetical glyci
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Mol. Microbiol. 18, 703-714, 1995
A;Title: Mechanism of antigenic variation in Mycoplasma pulmonis: interwoven, site-specia; Reference number: S70790; MUID:96414471
A;Reference number: S70791
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A; Accession: T31328
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A; Residues: 1-555 <BHU>
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cession: S70791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGYGSDSAAAAAAAAAAAAAAGG-ARGSGGYGGYGSDSAAAAAAAAAAAAAAAAAGSGAGGYGGG 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVNGD---VAKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNAAGAEGTINADAGKL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAA-----IGD 132
                          --ASVNGIAKGIKGIVDAA--GKADAKEGKLDATGAEGTTNVNAGKLFVKRAAD-----
                                                                                     KNNAGDANAGEMGKNNAGDANAGEMGKNNA----GDANAGDMGKNNAGDANAGEMGKNNA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAAASGAGGSGGG-----YGWGDGGYGSDSAAAAAAAAAAAAAAAGSGAGGAGGGYGWGD 1006
                                                                                                                                                KNNDHDNHKGTV-KNAVDMAKAAEEAASAASAATGNAATGDVVKNSGAAAKGGEA---- 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKAAABAASAATGSAAIGDVVNGNGATAKGGDAKSVNGIAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGDNDAAAAFATMKKDDQIAAAMVLRGMA-----KDGQFALKDAAAAHEGTVKNAVDI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YGWGDGGYGSDSAAAAAAAAAAAAAGSG-----AGGRGDGGYGSGSSAAAAAAAAAAAA 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVKNAGNVGGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRINPIDAAI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAAAAAAAAGSGAGGRGDGGYGSGSSAAAAAAAAAAAAAARR-AGHDSAAGSAAAAAAA 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRAGHDRAAGSAAAAAAAAAAAAASGAGGSGGGTGWGDGGTGSDSAAAA
                                                                                                                                                                                                                         101;
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                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: U23947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.6%;
                                                                                                                                                                                                            13.2%; Score 225.5; DB 2; 27.2%; Pred. No. 3.8e-05; tive 40; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 250; DB 2; Length 26; Pred. No. 8.1e-06; 25; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NID: g780764; PIDN: AAB41030.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2639;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PID: 9780766
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                                                                                                                                                                                                                  69;
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outer membrane lipoprotein - Borrelia hermsii
C;Species: Borrelia hermsii
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 08-Oct-1999
C;Accession: I40304
R;Restrepo, B.I.; Kitten, T.; Carter, C.J.; Infante, D.; Barbour, A.G.
Mol. Microbiol. 6, 3299-3311, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
I40304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Subtelomeric expression regions of Horrelia A;Reference number: I40300; MUID:93133110 A;Accession: I40304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: vmp25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:L04787; NID:g144029; PIDN:AAA22965.1; PID:g144030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-362 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated from GB/EMHL/DDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 99; Conserv
314 DKVVQSAGVTAVNKLLVAVEGIIKKTVKNVLEKAKGEIDKARAPK-ATG
                                                                                                                                                                                                                                     199
                                                                                                                                                                                                                                                                                                                                                        139
                                                                                                                                                                                                                                                                                                                                                                                                                 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 GKNNAGDANAGDMGKNNAGDANAGEMGKNNAGDANAGEMGKNNAGD-ANAGEMGKNNAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 GDANAGDMGKNNAGDANAGEMGKNNAGDANAGEMGKNNAGDANAGEMGKNNAGDANAGEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAVEAGKDGAAAATGGRSLSEVLMEVGKSAE-----NAFYSFMALVPDTLGLRVTKDT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKNNAGDANAGE 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLDATGAEGTTNVNAGKLFVKRAADD------GGDADDAGKAAAAVAASAATGNA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNGNGATAKGGD 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QILKAIVHAAKDGGEKQGKKAAD-----RTNPIDAAIGGAGDNDAAAAFA-TMKKDDQ
                                                                                                                                                                     KQGKKAADRTNPIDAAIGGAGDNDAAAAFATMKKDIQIAAAMVLRGMAKDGQF-----
                                                                                                                                                                                                                               DTAVKIGNADNKDGAKVLAA-AANAGRAVGD--KAAAIVSAVSGEEMLASIV--ASQEGD 253
                                                                                                                                                                                                                                                                                        -NAAGAEGTTNADAGKLFVKNAGNVGGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDGGE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKNEVG--GYFNSLGGKL--GKASDELEEVAKKSEVEGAKDGPIAVAIRAAVDTAKTTLS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAAEEAASAASAATGNAAIGDVVKNSGAAAKGGEAASVNGIAKGIKGIVDAAGKADAKEG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDAAEKADAKEGKLNAA--GAEGTTNADAGKLFVKNAGNVGGEAGDAGKAAAAVAAVSGE
                                                                                                                                                                                                                                                                                                                                                        TLKEHLESLKGIGDDDKVGEATSNQNGVAASTDELKGAFKALKGIVDTAGKEGVAKPKAG 198
                                                                                                                                                                                                                                                                                                                                                                                                           -----AIGDVVN-GDVAKAKGGDAAS---VNGIAKGIKGIVDAAEKADAKEGKL- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAAMVLRGMAKDGQFALKDAAAAHEGTV--KNAVDIIKAAAEAASAASAATGSAAIGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----NAGEMGKNNAGDANAGEMGKNNAGDANAGEMGKNNAGDANAGEMGKNN-
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                                                                                                               ADAALAADATAQTSALKFARGGGNAGQLAKEAAKAAAVAGGIALRSLVKGGKLAANNNDD
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                                                      -----ALKDAAAAHEG----TVKNAVDIIKAAAEAASAASAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.1%; Score 224.5; DB 2 ilarity 28.4%; Pred. No. 2.9e-05; Conservative 37; Mismatches 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148;
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361
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A;Residues: 1-364 <BUR>
A;Cross-references: GB:M57256; EMBL:X53927; NID:g144025; PIDN:AAB59031.1; PID:g144026
                                                                                                                                                                                                                                                                                                                                                                                                                                         variable major protein 21 - Borrelia hermsii C;Species: Borrelia hermsii C;Species: Borrelia hermsii C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change C;Accession: S11981 C;Accession: S11981 R. man, N.; Bergstroem, S.; Restrepo, B.I.; Barbour, A.G. Microbiol. 4, 1715-1726, 1990
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S11981
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                                                                                                                                      DЬ
                                                                                                                                                                    ΩV
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C;Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-246 <BAR>
A; Cross-references: GB: Z11876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Borrelia hermsii
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Mar-1993
C;Accession: A43579
                                                                                                                                                                                                                                                                                                                                                                     A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Barbour, A.G.; Carter, C.J.; Burman, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Comment: This spirochete eludes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     mman, N.; Bergstroem, S.; Restrepo, B.I.; Barboux
Microbiol. 4, 1715-1726, 1990
Le: The variable antigens Vmp7 and Vmp21 of the
ference number: S11980; MUID:91171872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein homolog - Borrelia hermsii
ecies: Borrelia hermsii
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                                                                                                                                                                                                                                  Local Similarity
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                                                            NSEAGIEKNDASKNPIRSAVNAAKKTLEALKGYLDSLGTV-
                                                                                                                                                                        VDMAKAAEEA-----ASAASAATGNAAIGDVVKNSGAAAKGGEAA-----
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GVAGTGIESLTKGIKAIVDVVLGKEGNAEAGTDKKAEDLSARTAAG--NGEAGKLFAANA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGDAASVNGIAKGIKGIVD-----AAEKADAKEGKLNAAGAEGTTNADAGKLFVKNA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGNPNASATETAVKTLIDNTLD------KIIEGSKTVSDAIGDASDPIANVGANNAA 54
                                                                                                                                                                                                                                                                                                                                                                   preliminary
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                                                                                                                                      MEVGKSAENAFYSFLELVSDTLGFTAKSTTKKEDVGGYFNSLG--GKLGEASNELEQVAK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASAATGSAAIGDVVNGNGATAKGGDAKSVN 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDAAAAFATMKKDDQIAAAMVLRGMAKDGQFALKDAAAAHEGTVKNAVDIIKAAAEAASA 314
                                                                                                -SVNGIAKG-----IKGIVDAAGKA-DAKEGKLDATGAEGTTNVNAGKLFVKRAADDGG 107
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31.9%;
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25.9%;
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Pred. No. 3.7e-05;
                                                                                                                                                                                                                                Score 215.5; DB 2
Pred. No. 8.5e-05;
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J. Biol. Chem. 263, 5495-5498, 1988
A;Title: Circumsporozoite protein gene from A;Reference number: A28615; MUID:88186854
A;Accession: A28615
A;Molecule from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
A60610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA.
A; Residues: 93-485 < LAL>
A; Residues: 93-485 < LAL>
A; Cross-references: GB:J03203; NID:g160212; PIDN:AAA29553.1; PID:g160213
C; Superfamily: Circumsporozoite protein; thrombospondin type 1 repeat hom C; Keywords: sporozoite; surface antigen; tandem repeat F; I-20/Domain: signal sequence #status predicted < SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            circumsporozoite protein precursor - Plasmodium bra
C;Species: Plasmodium brasilianum
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: A60610; A28615
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                                    GOFALKDAA-AAHEGTVKNAVDIIK-AAAEAASAASAATGS 321
                                                                                                                                                            GNAA-GNAA-GNAAGNDAGNAAGNAAGNAAG-----NAAGNA-AGNAAGNAAGNAA
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                                                                               GNAAGNAAGNAAGNAAGNAAGNAAGNAAGNAAGNEKAKNKDNKVDA---
                                                                                                                   KD-GGEKQGKKAADRT-NPIDAAIGGAGDNDAAAAFATMK----KDDQIAAAMVLRGMAKD
                                                                                                                                                                                                                                                                                                                                                                                                          NQEENNDSSNGPSEEHIKNYLESIRNSITEEWSPCSVTCGS
                                                                                                                                                                                                EGTTNADAGKLFVKNAGNVGGE------AGDAGKAAAAVAA--VSGEQILKAIVHAA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
107; Conser
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Pred. No. 0.00014;
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A; Experimental source: C; Genetics:

strain H37Rv

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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; A;Title: Deciphering the biology of Mycobacterium A;Reference number: A70500; MUID:98295987
A;Accession: B70807
                                                                                                                                                                                                                         R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
B70807
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C;Accession: E70917
C;Accession: E70917
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Squares, S.
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                                                                                                                                                                                                                                                                                                        hypothetical glycine-rich protein Rv3512 - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: B70807
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                                                  A; Molecule type: DNA
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A; Accession: E70917
     A; Cross-references:
                             A; Residues: 1-1079 <COL>
                                                                          A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: preliminary; nucleic acid sequence not shown; translation not shown
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ms-references: GB:Z95844; GB:AL123456; NID:g3250713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erimental source: strain H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGAGGKGGNGGLVGNGGAGGKGGDGMA--GVA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGGNGGAGGMGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNVGGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPIDAAIGGAGD 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGGNGGNGATGATGLNGLGAGADGTDGGKGGNGGAGGGGGGAGGQGGKALAATHQDGSMGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDVAKA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASAATGSAAIGDVVNGNGATAKGGDAKSVNGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDAAAAFATMKKDDQIAAAMVLRGMAKDGQFALKDAAAAHEGTVKNAVDIIKAAAEAASA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNAAGAEGTTNADAGKLFV-----KNA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AHGAAGASPTSGGNGGAG----GNGAHFSSGGKAGGNGGAGGAGGLYGNGG-----AGGA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
GB:AL022022;
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26.4%;
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GB:AL123456; NID:g3261554; PIDN:CAA17749.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 208; DB 2;
Pred. No. 0.00067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 162;
                                                                                                                                                    Whitehead, S.; Bastuberculosis from
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PID:g292444
                                                                                                                                                                                                                                                      Holroyd,
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                                                                                                                                                                                                                                                                              Gordon,
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C;Genetics:
A;Gene: Rv3512
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo
circumsporozoite protein precursor - Plasmodium cynomolgi (strain Ceylon)
N;Alternate names: major sporozoite surface intigen
C:Species: Plasmodium cynomolgi
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 07-Nov-1997
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                                                                                                                                                              AATAGSNGGAGTGSA-----GGNGGTGGRGGSGGAGGD--GIGGVGGG
                                                                                                                                                                                                     AAEAASAASAATGSAAIGDVVNGNGAT----AKGGDAKSVNGIAKG
                                                                                                                                                                                                                                                                                                                                                                                                    AGNG----GD-----GGDGAA------GAVGISGATGAGDGGHGGTGAAGGNGGTGGAGG
                                                                                                                                                                                                                                            GIGGKGGN-AGAGGAAGSNGGTVGA----NGTGGDG-----GNGGAA----
                                                                                                                                                                                                                                                                               AIGGAGDNDAAAAFATMKKDDQIAAAMVLRGMAK )GQFALKDAAAAHEGTVKNAVDIIKA
                                                                                                                                                                                                                                                                                                                        SGIDGVGGGTGGTGGNGGN--GAIGGAGGD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---AGGAGGNGGK-GGDGGAGVTSSTAGN--SGGAGGSGGKGGDAG-AGGAGATPGANGI 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDAAGKADAKEGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTAGTGGDGGKGGNGGIGAAGTTGPVGTGASGGTGGSGGAGGTGGDGGAANGGTAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTVKNAVDMAKAAEEAASAA--SAATGNAAIGDVVKNSGAAAKGGEAASVNGIAKGIKGI 67
                                                                                                                                                                                                                                                                                                                                                             KLFVKNAGNVGGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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F:1-19/Domain: signal sequence #status predicted <SIG>F:20-398/Product: circumsporozoite protein #status predicted F:97-240/Region: 9-residue repeats
F:241-991/Region: 17-residue repeats
F:323-376/Domain: thrombospondin type 1 repeat homology <THR1 R:Galinski, M.R.; Arnot, D.E.; Cochrane, A.H.; Barnwe Cell 48, 311-319, 1987
A;Title: The circumsporozoite gene of the Plasmodium A;Reference number: A90889; MUID:87102878
A;Accession: C26255 obic membrane-anchoring sequence.

C;Comment: There are 16 tandem copies of a 9-residue repeat and 3 copies
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat hom
C;Keywords: sporozoite; surface antigen; tandom repeat A;Residues: 1-398 <GAL> C;Comment: There are three distinct regions in the mature circumsporozoite protein, A; Molecule type: DNA A; Residues: 1-398 <G C; Accession: C26255 Cochrane, A.H.; Barnwell, J.W.; Nussenzweig, cynomolgi <THR1>

В δÃ 망 Qy Query Match Best Local S Matches 86 157 101 84 Local Similarity 34.8 nes 86; Conservative 27 AAAGEAGNNAAAGEAGNNAAAGEAGNNAAAGEAGNNAAAGEA---TGAEGTTNVNAGKLEVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDVAKAKG GGAAG-NNAAAGEAGNNAAGGAAGNNAAAGEAGNNAAAGGAAGNNAAAGEAGN---SAASAATGNAAIGDVVKNSGAAAKGGEAA---SVNCIAKGIKGIVDAAGKADAKEGKLDA 83 12.0%; Score 204.5; I Pred. No. 0.000 14; Mismatches .00035; DB 1; Length 398; Indels 39; -GNNAA 156 -NAAG Gaps 143 211 10;

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RESULT 12
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C;Superfamily:
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R; Cale, S.T.; Brosci
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A; Residues: 1-1901 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: F70806
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;Species: Mycobacterium tuberculosis
;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        722 V-----GGTNGSGGAGGAGGKGGTGGAGGSGADN------PTGAGFAGGAGGTGGAAGAG
                                                                                                                                         323 AIGDVVNGNGAT-AKGGDAKSVNG 345
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                                                                                                                                                                                                                                                                                            AAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPIDAAIGGAGDNDAAAAFATMKKDD
                                                                                                                                                                                                                                                                                                                                 GQGGAGGSAGAGGINGAGGAGGNGGDGGDGATGAAGLGDNGGVGGDGGAGGAAGNGGNAG
                                                                                                                                                                                                                                                                                                                                                                                                              GAGGATGTGGTGGVVGATGSAGIGGAGGRGGD-----GGDGAS--GLGLGLSGF-DGGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IAKGIKGIVDAAGKADAKEGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSVGNAGIGGTGGVGGAGGAGAAAAAGSSATGGAGFA----GGAGGEGG-AGGNSG
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                                                                                                   TLG -- VGGSGGTGGDGGDAGSGGG
                                                                                                                                                                             -----QGGAGGQGGQGGLGGASTTSINANGGAGGNG
                                                                                                                                                                                                                                                                                                                                                                         ----KADAKEGKLNAAGAEGTTNADAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106;
  glycine-rich protein Rv2490c - Mycobacterium tuberculosis (strain H37RV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.0%;
                                                                                                                                                                                                                                                        -----DGG-----AAGNGGNGGAGGAGGAGDNNFNGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 204.5;
Pred. No. 0.0
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                                                                                                     982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GNNAAAGAAG - NNAAAGEAGAGGAGRAGNNAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not shown; translation
                                                                                                                                                                                                                                                                                                                                                                       ---KLFVKNAGNVGGEAGDAGKAA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1901;
                                                                                                                                                                             ----GTGGKGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117;
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C;Species: Mycobacterium tuberculosis
C;Jate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Jate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: A70869
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go
R;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete
A;Reference number: A70800; MUID:98295987
A;Accession: A70869
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Best Local
1031
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                                                                                                                                     290 AAAAHEGTYKNAVDIIKAAAEAASAASAATGSAAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             693 GKGGAGGNGGLVGDGGAGGDGGSGAAGANGANVGEDGADGTLSGQPGEGSEANGGQGGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          633 DGDGGAGGDPGAGGKGGAGGAGATEGVTGATGATVHSGGNGGKGGNGADATVAGANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   753 GGGAGGAGGDGGAGSSALGSGGNGGRGDAGQAGGAGGAGGAGGAGGSVSGDGGPGGKGGA
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  AGGAGGSVSG
                                                                                                                                                                                                                                                                                                                         EAGDAGKAAAA-----VAAVSGEQILKAIVHAAKDGGE-KQGKKAADRTNPIDAAI
                                                                                                                                                                                                                                                                                                                                                                          GGAGGAGASGGGGGKGASG-ADSAE----
                                              KGGDAKSVNG
                                                                                         GGAGGNGG---
                                                                                                                                                                                   GGLGGDSGNGTRAASGVDASDHGPGSGGNGGNGGNGAQASVAGGAGGNGGDGGNAGRVGD
                                                                                                                                                                                                                                 GGAG - - - DNDAAAAFATMKKDD - - - - -
                                                                                                                                                                                                                                                                           PGGDGGAGGAAPAGQVGSHGVGGVGGDGGLGGAGGNGGDGGHGSDGGDGGDGGDPGAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                     KAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNAAGAEGTTNADAGKLFVKNAGNVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -NGIAKGIKGIV------DAAGKADAKEGKLDATGAEGT-----TNVNAGKLFV- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114;
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1040
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                                                                                         -DGAAGANGANSGAPGSDALALGQPGGNGGQGDAGQAGGAGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 202; DB 2; Pred. No. 0.0017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GKAAAAVAASAATGNAAIGDVVNGD-----VA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                 ·----QIAAAMVLRGMAKDGQFA--LKD
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circumsporozoite protein - Plasmodium malariae (strain Uganda 1-CDC) (;Species: Plasmodium malariae (;Species: Plasmodium malariae C;Date: 06-Oct-1994 #sequence_revision 04-Nov-1994 #text_change 20-A C;Accession: A54504

#text_change 20-Aug-1999

McCutcha

13

1. A.A.; de la Cruz, V.F.; Campbell, G.H.; Procell, P.M.; Collins, W.E.; Biochem. Parasitol. 30, 291-294, 1988

gene of

Plasmodium malariae

A;Cross-references: GB:J03992; NID:g160220; PIDN:AAA29557.1; C;Superfamily: circumsporozoite protein; thrombospondin type

PID:g160221 1 repeat homology

A; Molecule type: DNA A; Residues: 1-429 <LAL>

A; Title: Structure of the circumsporozoite A; Reference number: A54504; MUID:89040027 A; Accession: A54504

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Proc. Natl. Acad. Sci. U.S.A. 87, 7120-7124, 1990
A;Title: Structure of a protein superfiber: spide:
A;Reference number: A36068; MUID:90384959
A;Accession: A36068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           major ampullate fibroin protein - orb spider (Nephila clavipes) (fragment) C;Species: Nephila clavipes C;Date: 08-Mar.1991 #sequence_revision 13-Jan-1993 #text_change 09-Sep-1997 C;Accession: A36068
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A36068
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A; Molecule type: DNA
A; Residues: 1-718 <XUA>
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Best Local
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Best Local
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le: the authors translated the codon GGT for residue
                                               410
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                                                                                                                                      124
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                  231 GEKQGKKAADRTNPIDAAIGGAGDN-
                                                                                                                                                                   294
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                                                                                                                                                                                                                                          20 KAAEEAASAASAATGNAAIGDV-VKNSGAAAKGGE-----AASVNGIAKGIKGIVDAAGK 73
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                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNPIDAAIGGAGDNDAAAAFATMKKDDQIAAAMVLRGMAKDGQFALKDAAAAHEGTVKNA 301
                                                                       GKLNAAGAEGTTNADAGKLFVKNAGNVGGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDG 230
                                                                                                      GGLGSQGAGRGGLGGQGAGAVAAAAAGGAGQGGYGGLGSQGAGRGGQG----AGAAAAAA 409
                                                                                                                                                               GQGGYGGLGSQGAGRGGLGGQGAGAAAAGGAAQGGLGGQGAGQAAAAAAAAGGAGQGGY 353
                                                                                                                                                                                           ADAKEGKLDATGA--EGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASA-----
                                                                                                                                                                                                                        QGAGQGAGASAAAAGGAGQGGYGGLGSQGAGRGGEGAGAAAAAAAGGAGQGGYGGLGGQGA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NDHDNHKGTVKNAVDMAKAAEEAASAASAATGNAAIGDVVKNSGAAAKGGEAASVNGIAK 62
                                            GGAGQRGYGGLGNQGAGR-----GGLGGQG--AGAAAAAAAGGAGQGGYGGL---GNQG 458
                                                                                                                       -----ATGNAAIGDVVNGDVAKAKGGDAA------SVNGIAKGIKGIVDAAEKADAKE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNKVDA------NTNKKDNQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LESIRNSITEEWSPCSVTCGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 11.8%; Score 201.5; DB 2; Similarity 30.2%; Pred. No. 0.00053; 97; Conservative 26; Mismatches 135;
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                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                  11.5%;
26.1%;
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                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                    164; Indels
--DAAAAFATMKKDDQIAAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                dragline
                                                                                                                                                                                                                                                                                                              Length 718;
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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: E70806
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C;Superfamily: collagen alpha 1(IV) chain
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A;Molecule type: DNA
A;Residues: 1-1381 <COL>
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Best Local Similarity
Matches 107; Conserv
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14; Mismatches 163
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Search completed: January 10, 2002, 14:04:28 Job time: 122 sec

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B 8

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44 NSGAAAKGGEAASVNGIAKGIKGIVD------AG-KADAKEGKLDA--TGAEGT

89

NSGGVAEDPKTVYLTSIANLGKGFLDVFVTFGDMYTGAFGIKADTKKSDIGKYFTDIEST

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01-OCT-1993 (Rel. 27, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
VARIABLE MAJOR OUTER MEMBRANE LIPOPROTEIN 25 PRECURSOR
VMP25
                                                                   SEQUENCE
                                                                                                                       SIGNAL
                                                                                                                                                                                        EMBL; L04787; AAA22965.1; -
                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                           Mol.
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Restrepo B.I., Kitten T., Carter
"Subtelomeric expression regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia hermsii.
                                                                                                                                  Outer membrane;
                                                                                                                                                  PROSITE;
                                                                                                                                                                Pfam;
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                                                                                                                                                                           [nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
                                                                                                                                                                                                                                                                                                                                                             highly polymorphic.";
. microbiol. 6:3299-3311(1992).
FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY CHANGING FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
                                                                                                                                                                                                                                                                                                                         SIMILARITY: STRONG, TO VMP7 AND VMP21.
                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: ATTACHED
                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                        ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAAAEAASAASAATGSAAIGDVV-----NGNGATAKGGDAKSV 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNAAGAEGTTNADAGKLFVKNAGNV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MTSVKKKLQDEVAKNGNYPKVKTAVDEFVAILGKIEKGAKEASKGATGDVIIGNTVKNGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RADNAAAQAAAASIGAVTGADILQAIVQSKENPVANSTDGIEK-----ATDAAEIAVA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGEAGDAGKAAAAVAAVSGEQILKAIVHA-----AKDGGEKQGKKAADRTNPIDAAIG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAKDNKKEIKDGA-----KKDAVIAAGIALRAMAKNGTFSIKNNEDA-----
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                                                                                                                                                 PF00921; Lipoprotein_2;
TE; PS00013; PROKAR_LIPO
    99;
               Similarity
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                                                              27
362
                                                                                                                                                                         IPR000680; Borrelia_lipo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HS1 SEROTYPE 25;
  Conservative
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                                                                                                                                  Lipoprotein; Signal; Plasmid
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                                                                                                                                                PROKAR_LIPOPROTEIN; 1.
                                                                                                         362
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36468
             13.1%;
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X
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 37;
Score 224.5;
Pred. No. 7.3e
37; Mismatches
                                                                  N-ACYL DIGLYCERIDE 2A3EF5248D5637FD
                                                                                           VARIABLE MAJOR OUTER MEMBRANE LIPOPROTEIN 25.
                                                                                                                       PROBABLE.
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TO THE OUTER MEMBRANE BY
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            3e-05;
                        DB 1;
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hermsii linear plas
                                                                  (PROBABLE)
CRC64;
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Indels
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RESULT 3
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                                                                                                                                                                                           MEDLINE-85236116; PubMed-2409197;
Barstad P.A., Coligan J.E., Raum M.G., Barbour
"Variable major proteins of Borrelia hermsii.
partial sequence analysis of CNBr peptides.",
J. Exp. Med. 161:1302-1314(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91171872; PubMed-1706456;
Burman N., Bergstroem S., Restrepo B.I., Barbour A.G.;
"The variable antigens Vmp7 and Vmp21 of the relapsing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1991 (Rel.
01-MAY-1991 (Rel.
01-FEB-1994 (Rel.
              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                    Restrepo B.I., Kitten T., Carter C.J., Infante D., Barbour A.G.; "Subtelomeric expression regions of Borrelia hermsii linear plasmids are highly polymorphic."; mol. Microbiol. 6:3299-3311(1992).
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM STRAIN-SSP. HS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins of the African trypanosome."; Mol. Microbiol. 4:1715-1726(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SSP. HS1 SEROTYPE 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borrelia hermsii.
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                                                                                                                                                                                                                                                                                    SEQUENCE OF 55-75; 186-208 AND 245-259.
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93133110; PubMed=1484486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacterium Borrelia hermsil are structurully analogous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254
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European Bioinformatics Institute. To
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                                                                                                                                       FÜNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY CHANGING FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPII
                                                                                                      SIMILARITY: STRONG,
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                                                                                                                                                                                                                                                                                                                                                                                                          OM N.A.
HS1 SEROTYPE 21;
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18, Last sequence update)
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7TER MEMBRANE LIPOPROTEIN 21
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RESULT 4
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P14593;
                                                                                                                                                                                                                                                                     ### Jan-1990 (Rel. 13, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) CIRCUMSPOROZOITE PROTEIN (CS) (FRAGMENT).
                                                                             "Circumsporozoite protein gene from Plasmodium brasilianum. Anim reservoirs for human malaria parasites?";
J. Biol. Chem. 263:5495-5498(1988).
-i- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PRAASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO TH
                                                                                                                                                             Lal A.A., la Cruz V.F., McCutchan T.F.;
                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-88186854;
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Pfam; PF00921; Lipoprotein_2; 1.
PROSITE; PS00013; PROKAR_LIPOPROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M57256; AAB59031.1; PIR; S11981; S11981.
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                                                                                                                                                                                                                                  NCBI_TaxID=5824;
                                                                                                                                                                                                                                             Eukaryota; Alveolata; Apicomplexa;
                                                                                                                                                                                                                                                          Plasmodium brasilianum
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)1-JAN-1990 (Rel.
20-AUG-2001 (Rel.
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or send an email to license@isb-sib.ch).
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              WOULD BE TH
SIMILARITY:
           ANCHORING THE PROTEIN TO THE CELL MEMBRANE. WOULD BE THE SURFACE ANTIGEN OF THE ORGANIS SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                    VERTEBRATE HOST)
MISCELLANEOUS: TI
                                                                                                                                                                                                                                                                                                                                                                                                                                           MAKDGQFAL - - KDAAAAHEG - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARPEVGNIAVKVGNGTDNKDGAKIL---ATDGAAAVGDAGKAAAILTTVSGKEMLASIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A---KEGKLNAAGAEGTTNADAGKLFVKNAGNVGGEAGDAGKAAAAVAAVSGEQILKAIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSNPVGWAS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DADDAGKAAAAVAASAATGNAAIGDVVNGDVAKAKGGDAASVNGIAKGIKGIVDAAEKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSEAGIEKNDASKNPIRSAVNAAKKTLEALKGYLDSLGTV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEVGKSAENAFYSFLELVSDTLGFTAKSTTKKEDVGGYFNSLG--GKLGEASNELEQVAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSTEDKAVKITGNVTVETTPLEFAVGGNGAHLSQNANSKAAA------VAGGIALRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SVNGIAKG-----IKGIVDAAGKA-DAKEGKLDATGAEGTTNVNAGKLFVKRAADDGG 107
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364
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                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----NNAQGAAV-----DEAELKKAYKALKGIMDTAEGAG
                                                                                                                                                                                         PubMed=3128542;
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                                                    THE C-TERMINAL REGION IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ASAASAATGNAAIGDVVKNSGAAAKGGEAA-----
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37084
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25.9%;
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                                                                                                                                                                          Collins W.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIPOPROTEIN 21.
N-ACYL DIGLYCERIDE
; 16598B639EE63776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal; Plasmid PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIABLE MAJOR OUTER
                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e 215.5; DB
                                                                                                                                                                                                                                              Haemosporida;
                                                                                                                                                                                                                                                                                                                                           393
                                                                                                                                                                           Campbell G.H.,
                           ORGANISM.
                                                                                                                                                                                                                                                                                                                                           AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                    PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                                                          -TVKNAVDIIKAAAEAA
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CRC64;
                                         THE
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                                         REPEAT
                                                                                                                                                                           Procell P.M.,
                                         SEQUENCES
                                                                                                                                                 Animal
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Best Local S
Matches 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence upda)
20-AUG-2001 (Rel. 40, Last annotation upo
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
Plasmodium cynomolgi (strain Ceylon).
Eukaryota; Alveolata; Apicomplexa; Haemoo
                                                                                                                                                                                                                                                                 CSP_PLACC P08673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00090; tsp_1; 1.
SMART; SM0209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
                                                                  "The circumsporozoite gene of the Plasmodium cynomolgi complex."; Cell 48\colon 311 \cdot 319 (1987).
                                                                                              Galinski M.R., Arnot D.E.,
Nussenzweig R.S., Enea V.;
                                                                                                                        MEDLINE=87102878; PubMed=3802196;
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                 NCBI_TaxID=5829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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Local Similarity 31.4%;
nes 107; Conservative 2
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                          MISCELLANEOUS: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                        Ç
 MISCELLANEOUS:
              VERTEBRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNNDHDNHKGTVKNAVDMAKAAEEAASAASAATGNAAIGDVVKNSGAAAKGGEAASVNGI 60
                                                                                                                                                                                                                                                                                                                                                                            GQFALKDAA-AAHEGTVKNAVDIIK-AAAEAASAASAATGS 321
                                                                                                                                                                                                                                                                                                                                                                                                        GNAAGNAAGNAAGNAAGNAAGNAAGNAAGNAAGNEKAKNKDNKVDA----NTNKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASAATGNAAIGDVVNGDVAKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNAAG--A 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NQEENNDSSNGPSEEHIKNYLESIRNSITEEWSPCSVTCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                    KD-GGEKQGKKAADRT-NPIDAAIGGAGDNDAAAAFATMK----KDDQIAAAMVLRGMAKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKGIKGIVDAAGKADAKEGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVA 120
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               HOST)
                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                 06, Created)
06, Last sequence update)
40, Last annotation updat
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THE C-TERMINAL REGION IS
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                                                                                                             Cochrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 213.5; DB 1
Pred. No. 0.00027;
8; Mismatches 163
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B32944419BC600AA CRC64;
                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                               Haemosporida;
                                                                                                           А.Н.,
                                                                                                                                                                                                                                                                              398
                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                              AΑ
                                                                                                             Barnwell J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
 PROBABLY USED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163;
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                                                                                                                                                                               Plasmodium
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RESCUT 6

YZ.08_M AYCTU
ID YZ.08_M
AC 053553
DT 30-MAY
DT 30-MAY
DT 20-AUG
DE HYPOTH
GN RV3508
OS MYCODB
OC ACTINC
OX NCBI_T
RN [1]
RN [1]
RN SEQUEN
RX MEDLII
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Best Local S
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053553;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seque
20-AUG-2001 (Rel. 40, Last annot
HYPOTHETICAL PE-PGRS FAMILY PROT
RV3508 OR MTV023.15.
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SMART; SM00209; TSP1; 1.

Malaria; Sporozoite; Repeat; Signal SIGNAL 1 19 PROBABI CHAIN 20 398 CIRCUM: DOMAIN 97 249 17 x 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The state are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
          MEDLINE~98295987;
                                               STRAIN-H37RV;
                                                                                                                                                                                                         Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                              SEQUENCE FROM N.A
                                                                                                                                        NCBI_TaxID=1773;
                                                                                                                                                                          Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003067; Crcmsprzoite
InterPro; IPR000884; TSP1.
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SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKDGGEKQGKKAADRTNPIDAAIGGAGDNDAAAAFATMKKDDQIAAAMVLRGMAKDGQFA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAGNNAAGGEAGNNAAAGEAGNNAAAGGAAGNNAAAGEAGNNAAAGAAGN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- EAGAGGAGRAGNNAAAGEAGAGGAGRAGNNAAAGEAGAGG-AGGNAGNKKAGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGKLNAAGAEGTTNADAGKLFVKNAGNVGGE----AGDAGKAAAAVAAVSGEQIIKAIVHA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --DKPKKKDEKQVEPKKPRENKLKQPAGNNAAAGEAGNNAAAGEAGNNAAAGEAGNNAAA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKAAAAVAASAATGNAAIGDVVNGDVAKAKGGDAA---SVNGIAKGIKGIVDAAEKADAK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVDAAGKADAK-----EGKL-----DATGAEGTTNVNAGKLFVKRAADDGGDADDA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLNGVSFNNVDASSLG--AAQVRQSASRGRGLGENPKNEEGA--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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,
                                                                                                                                                                          Corynebacterineae;
          PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37718 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.3%; 27.2%;
                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
FAMILY PROTEIN RV3508 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 209.5; DB 1; Pred. No. 0.00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A-G-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIRCUMSPOROZOITE PROTEIN.
17 x 9 AA TANDEM REPEATS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6DFA2E8A62ED05BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1901
                                                                                                                                                                       Mycobacteriaceae; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AΑ
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                                                                                                                                                                       Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A-G-N-N-A-A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109;
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                                                                                                  RESULT 7
CSP_PLAMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    뫄
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                  CSP_PLAMA
P13815;
01-JAN-1990 (Rel. 13, Created)
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Best Local Si
Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; SIGNAL 1 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00934; PE; 1. ProDom; PD001223; PE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL022022; CAA17745.1; -. HSSP; P19972; 1KVD. Tuberculist; Rv3508; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterPro;
                               323 AIGDVVNGNGAT-AKGGDAKSVNG
                                                                                                                                                 269
                                                                                                                                                                                                                                                         209
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                                                                                                                                                                                                                                                                                                                                                                                                                771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 GTVKNA------VDMAKAAEEAASAASAATGNAAIGDVVKNSGAAAKGGEAASVNG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
TLG - - VGGSGGTGGDGGDAGSGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AASAATGNAAIGDVV------NGDVAKAKGGDAASVNGIAKGIKGIVDAAE- 164
                                                                                                                                                                                                      VGLTAKAG------DGG-----AAGNGGNGGAGGAGGAGDNNFNGG-----
                                                                                                                                                                                                                                                      AAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPIDAAIGGAGDNDAAAAFATMKKDD 268
                                                                                                                                                                                                                                                                                                                                                                                                          GAGGATGTGGTGGVVGATGSAGIGGAGGRGGD-----GGDGAS--GLGLGLSGF-DGGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSVGNAGIGGTGGVGGAGGAGAAAAAGSSATGGAGFA-----GGAGGEGG-AGGNSG
                                                                                                                                                 QIAAAMVIRGMA--KDGQFALKDAAA----AHEGTVKNAVDIIKAAAEAASAASAATGSA 322
                                                                                                                                                                                                                                                                                                        GQGGAGGSAGAGGINGAGGAGGNGGDGGDGGAGGAAGNGGNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IAKGIKGIVDAAGKADAKEGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAV 119
                                                                                                                                                                                                                                                                                                                                                        ----KADAKEGKLNAAGAEGTTNADAG------KLFVKNAGNVGGEAGDAGKAA 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GGTNGSGGAGGAGGKGGTGGAGGSGADN-----PTGAGFAGGAGGTGGAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1901 AA; 147627
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                                                                                                  QGGAGGQGGQGGLGGASTTSINANGGAGGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.0%;
27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat; Signal; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 204.5; DB Pred. No. 0.0029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL PE-PGRS FAMILY RV3508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
982
                                               345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136;
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                                                                                                  -GTGGKGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              tches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-89040027; PubMed-3054537;
Lal A.A., la Cruz V.F., Campbell
McCutchan T.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure of the circumsporozoite gene of Plasmodium malar Mol. Blochem. Parasitol. 30:291-294(1988).

-i- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOM SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STACE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO VERTEBRATE HOST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01303; CRCMSPR SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P04002; 1WFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J03992; AAA29557.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00090; tsp_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
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353
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                                                                                                                                                                                                                                173
                                                                                                                                                                                                                                                                                        63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SE WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.

SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A54504; A54504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN Buropean Bioinformatics Institute. There are no rest
                                                                                                                                NADAGKLFVKNAGNVGGEAGDAGKAAA-AVAAVSGEQILKAIVHAAKDGGEKQGKKAADR
                                                                                                                                                                                                                                                                                                                 NDHDNHKGTVKNAVDMAKAAEEAASAASAATGNAAIGDVVKNSGAAAKGGEAASVNGIAK 62
LESIRNSITEEWSPCSVTCGS
                          VDIIK-AAAEAASAASAATGS
                                                                                  TNPIDAAIGGAGDNDAAAAFATMKKDDQIAAAMVLRGMAKDGQFALKDAAAAHEGTVKNA 301
                                                                                                                                                                      AATGNAAIGDVVNGDVAKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNAAGAEGTT
                                                                                                                                                                                                                               GIKGIVDAAGKADAKEGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAAS 122
                                                                                                              NA - AGNAAGNAAGNA - - AGNAAGNAAGNAAGNAAGNAAGNAA - - GNAAGNEKAKNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sporozoite; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              16
110
429
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRCMSPRZOITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                   429
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30.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
373
                          321
                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                CIRCUMSPOROZOITE PROTEIN
4 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROBABLE
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                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                           201.5;
No. 0.0
                                                                                                                                                                                                                                                                                                                                                       , 0011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as its content
                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                               135;
                                                       EENNDSSNGPSEEH - - - IKNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE REPEAT SEQUENCES
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
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                                                                                                                                                                                                                                                                                                                                              63;
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MBL outstation -
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RESULT 8

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ID SPDI_N
AC P19837
AC P18337
AC P1
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P19837;
01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence conservation in the C-terminal region of spider silk proteins (Spidroin) from Nephila clavipes (Tetragnathidae) and Araneus bicentenarius (Araneidae).";
J. Biol. Chem. 269:6661-663(1994).
-i- FUNCTION: THIS SPIDER MAJOR AMPULLATE SILK POSSESSES UNIQUE CHARACTERISTICS OF STRENGTH AND ELASTICITY. IT MAY CONSIST OF PSEUDOCRISTALLINE REGIONS OF ANTIPARALLEL BETA-SHEET INTERSPERSED WITH ELASTIC AMORPHOUS SEGMENTS.
-i- SUBUNIT: MAJOR SUBUNIT, WITH SPIDROIN 2, OF THE DRAGLINE SILK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
SPIDROIN 1 (DRAGLINE SILK FIBROIN 1) (FRAGMENT).
Nephila clavipes (Orb spider).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beckwitt R., Arcidiacono S.;
"Sequence conservation in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 653-747 FROM N.A. MEDLINE=94165058; PubMed=8120021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure of a protein superfiber: spider dragline silk.";
Proc. Natl. Acad. Sci. U.S.A. 87:7120-7124(1990).
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                                                                                                                    Burman N., Bergstroem S., Restrepo B.I., Barbour A.G.; "The variable antigens Vmp7 and Vmp21 of the relapsing bacterium Borrelia hermsii are structurally analogous to proteins of the African trypanosome.";
                                                                                                                                                                                                                                                                                             01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last seq
01-OCT-1996 (Rel. 34, Last ann
                Restrepo B.I., Kitten T., Carter C.J. "Subtelomeric expression regions of are highly polymorphic.";
                                                                     SEQUENCE FROM N.A.
STRAIN-SSP. HS1 SEROTYPE
                                                                                                          proteins of the African trypanosome. Mol. Microbiol. 4:1715-1726(1990).
                                                                                                                                                                    MEDLINE-91171872; PubMed-1706456;
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                                 C.J., Infante D., Barbour l of Borrelia hermsii linear
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MEDLINE-85236116; PubMed-2409197;

Barstad P.A., Coligan J.E., Raum M.G., Barbour A.G.;

"Variable major proteins of Borrella hermsil Epitope mapping
partial sequence analysis of CNBr peptides.";

J. Exp. Med. 161:1302-1314(1985).

-I- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY CHANFROM ONE SURFACE EXPOSED VMP TO ANOTHER.
                      STFR_ECOLI STANDARD; PRT; 1120 AA. P76072; P77560; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) STDE TAIL FIBER PROTEIN HOMOLOG FROM LAMBHOOID STFR OR B1372.
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  Escherichia
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MEDLINB-97426617; PubMed-9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perr

Riley M., Collado-Vides J., Glasner J.D., Rode C

Gregor J., Davis N.W., Kirkpatrick H.A., Goeden
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                                                                                                                                                                                                                                                                                                                                                                          GIVDAAGKADAKEGKLDATG----AEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAA 121
DASTTKKGIVQ-----LSSATNSTSETLAATPKAVKSAYDNAEKRLQKDQNGADIPDKGC
                                        DAAAAHEGTVKNAVDIIKAAAEAASAASAATGSAAIGDVVNG-----NGATA--KGG
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                                                                                    ATTASTKATEAAGSATAAAQSKSTAESAATRAETAAKRAEDIASAV---
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cal protein; Fiber protein; Repeat; Complete proteome
1120 AA; 113779 MW; 542E59D71EE795B4 CRC64;
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Pred. No. 0.
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30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV0747
RV0747 OR MT0772.5 OR MTV041.21.
                                                                                                                                                                                  Hypothetical protein; Repeat; SIGNAL 1 30
                                                                                                                                                                                                                     InterPro; IPR000084; PE. Pfam; PF00934; PE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laboratory strains.";
Submitted (APR-2001) to
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Fotonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                            TubercuList; Rv0747;
                                                                                                                                                                                                                                                                                                    EMBL; AL021958; CAA17514.1; EMBL; AE006968; AAK45011.1;
                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
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SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
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                                                                                                                                                                            Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr Gordon S.V., Elgimeter K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Ouail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
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CONFLICT
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01-NOV-1997 (Rel. 35, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV
RV2634C OR MT2712 OR MTCY441.04C.
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YQ34_MYCTU
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White (Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzbe Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Miku
                                                                                                         SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-H37RV;
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NCBI_TaxID=1773;
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Bacteria; Firmicutes; Actinobacteria;
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Submitted (APR-2001) to
-!- SIMILARITY: BELONGS
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[1]
SEQUENCE FROM PSTRAIN-JM105;
STRAIN-JM105;
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EMBL;
EMBL;
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                                                   or send
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                                                                                                                                                                                                                                                                                                                         MEDLINE-99332679; PubMed=10404600;
Lubkowski J., Hennecke F., Plueckthun
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Yano M., Horiuchi T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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                                                                                                          European
                                                                                                                                                                                                SUBUNIT:
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                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
M28232; AAA24683.1; -. AE000177; AAC73833.1; D90713; BAA35405.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natl. Acad.
                                                  opean Bioinformatics Institute. The non-profit institutions as long dand this statement is not removed is requires a license agreement (See an email to license@isb-sib.ch).
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ebster R.E.;
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01-OCT-1996 (Rel. 3
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DOMAIN
          MEDLINE=88330868; PubMed=2971041;
Deak S.B., Pierce R.A., Belsky S.A., F
"Rat tropoelastin is synthesized from
                                                              Biochemistry
                                                                         Pierce R.A., Deak S.B., Stolle C.A. "Heterogeneity of rat tropoelastin
                                                                                                                            Mammalia; Eutheria; NCBI_TaxID=10116;
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Mammalia;
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                                                            "Heterogeneity of rat tropoetast
Biochemistry 29:9677-9683(1990).
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                                                                                  PubMed=1702999;
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(TROPOELASTIN) (FRAGMENT).
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EMBL; J04035; AAA42268.1; -.
EMBL; M66372; AAA42271.1; -.
EMBL; M66375; AAA42271.1; JOINED.
EMBL; M6635; AAA42271.1; JOINED.
EMBL; M6636; AAA42271.1; JOINED.
EMBL; M6636; AAA42271.1; JOINED.
EMBL; M6636; AAA42271.1; JOINED.
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SEQUENCE OF 264-533 AND 558-864 FROM N.A.
MEDLINE=92241859; Pubmed=1572637;
Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.;
"Elements of the rat tropoelastin gene associated with alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS INCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED
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                                                                                                          VPGTGGVPGAGTPAAAAAAAAAAAKAAAKAGQYGLGPGVGGVPGGVGGVGGLPGGVGPGGVTG
                                                                                                                                                                           GGASQAAAAAAAAKAAKYGAGGAGTLGGLVPGAVPGALPGAVPGALPGAVPGALPGAVPG
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                                                                                                                                                                                                                                                                       GIAKGIKGIVD-----AAGKADAKEGKLDATGAEG--TTNVNAGKL---FVKRAADD 105
                                                                                                                                                                                                                                                                                                      AAAAKAAAKAAKYGAAGGLVPGGPGVRVPGAGIPGVGIPGVGGIPGVGGIPGVG 405
                                              IGTG----PGTGLVPGDLGGAGTPAAAKSA--AKAAAKAQYRAAAGLGAGVPGLGVGAGV 639
                                                                           ADAGKLFVKNAGNVGGEAGDAGKAAAAVAAVSGEQILKAIVHAAKD-GGEKQGKKAADRT
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protein; Connective tissue;
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MISSING (IN CERTAIN CLONES).
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Matches 113; Conser
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P54320;
01-OCT-1996
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MEDLINE-95130069; PubMed-7829060;
Wydner K.S., Sechher J.L., Boyd C.D., Pussmore H.C.;
"Use of an intron polymorphism to localize the tropoelastin mouse chromosome 5 in a region of linkage conservation with
                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for entities requires a license agreement (see http://www.isb-sib or send an email to license@isb-sib.ch).
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Genomics 23:125-131(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse chromosome 5 chromosome 7.";
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Mammalia; Eutheria;
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SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
AKAAKYGAGGAGALGGLVPGAVPGALPGAVPAVPG-AGGVPGAGTPAAAAAAAAAAAKAAAK
                          AAVAASAATGNAAIGDVVNGDVAKAKGGDAASVNGIAKGIKG-----IVDAAEKADAK 169
                                                     GPGAVSPAAAAKAAKYGARGGVGIPTYGVGACGFPGYGVGAGAGLGGASPAAAAAA
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|etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
|theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                AAGKADAKEGKLDATGAEG--TTNVNAKKL---FVKRAADDGGDADDAGKAA 116
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Search completed: January 10, 2002, 14:09:57 Joh time: 326 sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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235
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           US-09-708-427-66722
US-09-708-427-66721
US-09-708-427-28541
US-09-708-427-28539
US-09-708-427-22539
US-09-708-427-27506
US-09-708-427-27506
US-09-708-427-11856
US-09-708-427-11854
US-09-708-427-11854
US-09-708-427-11854
US-09-708-427-11854
US-09-708-427-11854
US-09-708-427-62406
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             sequence
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Sequence
Sequence
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NAME/KEY: misc_feature
LCATION: 1..312
OTHER INFONMATION: Ceres Seq. ID 1931146
US-09-708-427-66721
                                                                                                                                                                                                                                                                                       RESULT 4
US-09-708-427-28541
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APPLICANT: N. TEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

FILE REPERBNCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEO ID NOS: 85364

SOFTWARE: Patentin version 3.1

SEO ID NO 66720

LENGTH: 394

TYPE: PRT
                                                                                                                                                                                                                            Sequence 28541, Application US/09708427 GENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al.
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Best Local Similarity
Matches 12; Conserv
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                                                                          SEQ ID NO 28541
                                                                                          CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                    TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
FEATURE:
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OTHER INFORMATION: Xaa is
                                    LENGTH: 604
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..394
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE: misc_feature
FEATURE:
                ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Ceres Seq. ID 1931145
                                                                                                                                                                                                                                                                                                                                                                   318 PLQSCMNHSCRPNAKAFKRDEDKDGHAVITALRPISKDEEITI 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 PLQSCMNHSCRPNAKAFKRDEDKDGHAVIIALRPISKDEEITI 278
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 27.9 les 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     5 PIDAAIGGSADRNAEAFDKMKKDDQIAAAMVLRGMAKDGQFAL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 PIDAAIGGSADRNAEAFDKMKKDDQIAAAMVLRGMAKDGQFAL 47
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27.9%;
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Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 394; 16;
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US-09-708-427-28539
: Sequence 28539, Application US/09708427
: GENERAL INFORMATION:
: APPLICANT: N. ALEXANDROV et al.
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Best Local Similarity
Thehes 15; Conserve
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 28539
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Best Local (
                                                                                                                                                                                                                                                          TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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LOCATION: 1..604
OTHER INFORMATION: xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..604
OTHER INFORMATION: Ceres Seq. ID 1823502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa NAME/KEY: misc_feature LOCATION: 1..620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Arabidopsis thaliana
NAME/KEY: misc_feature
LOCATION: 1..686
OTHER INFORMATION: Xaa is any amino acid
                                                                                     ORGANISM: Arabidopsis thalians
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Ceres Seq. ID 1823501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1.620
                                                                                                               TYPE: PRT
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                                                                     FEATURE:
                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 PLANTLYNVYGKCGAASHALQVFDEMPHRDHIAWASVLTAL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 PLANTLVNVYGKCGAASHALQVFDEMPHRDHIAWASVLTAL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 PLTNPIDAAIG--GSADRNAEAFDKMKKDDQIAAAMVLRGM 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 PLTNPIDAAIG--GSADRNAEAFDKMKKDDQIAAAMVLRGM 39
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36.6%;
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Pred. No. 27;
5; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ب</u>
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; NUMBER OF SEQ ID NOS: 8409
; SEQ ID NO 5275
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Xenorhabdus sp.
US-09-897-516-5275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-09-897-516-5275
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; LOCATION: 1.686
; OTHER INFORMATION: Ceres Seq. ID 1823500
US-09-708-427-28539
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                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27506
LENGTH: 526
                                                                                                                                                                                                                                                                                                                                                                   Sequence 27506, Appl GENERAL INFORMATION:
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Best Local Similarity 39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 36.6%;
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                                                                                                                                                                                                                                                                                          APPLICANT: N. ALEXANDROV et al. TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome
FILE REFERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
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                  NAME/KEY: misc_feature
LOCATION: 1.526
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1.526
                                                                                                                FEATURE:
                                                                                                                                 ORGANISM: Arabidopsis thaliana
                                                                                                                                                         TYPE: PRT
OTHER INFORMATION: Ceres Seq. ID 1821102
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PLICANT: Goldman, Barry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 KNAKLYEAAKKADGTDGGYVIRGEDKDG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 PLANTLVNVYGKCGAASHALQVFDEMPHRDHIAWASVLTAL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 RNAEAFDKMKKDDQIAAAMVLRGMAKDG 43
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Hinkle, Gregory
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Pred. No. 1
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US-09-708-427-27504
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US-09-708-427-27505
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; OTHER INFORMATION: Ceres Seq. US-09-708-427-27504
                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 27504
LENGTH: 727
                                                                                                                                                                                                                                                                                                                    Sequence 27504, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS
TITLE OF INVENTION: THEREBY
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 27505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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Best Local Similarity

Matches 11; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 2750-1243P
                                  LOCATION: 1..727
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: 1..544
OTHER INFORMATION: Xaa is any amino
                                                                                                          NAME/KEY: misc_feature
                                                                                                                                            ORGANISM: Arabidopsis thaliana
                                                                                                                                                                        TYPE: PRT
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LOCATION: 1..544
OTHER INFORMATION: Ceres
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                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 GNLDASLRVWDEMRRDEIKPDVMAYGTLVVGLCKDGR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 GNLDASLRVWDEMRRDEIKPDVMAYGTLVVGLCKDGR 147
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29.7%;
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29.7%;
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Pred. No. 30;
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Pred. No. 32;
                ID 1821100
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US-09-708-427-11855
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al
                                                                                                                                                                                                                                                                     SEQ ID NO 11855
LENGTH: 1535
   Matches
                    Best
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Best Local Similarity
                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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PLICANT: N. ALEXANDROV et al.

TILE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

TITLE OF INVENTION: THEREBY

TITLE OF INVENTION: UNDER: US/09/708,427

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: Patentin version 3.1
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CURRENT FILING DATE: 2000-11-09
UMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 11856
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TYPE: PRT
                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 1..1535
OTHER INFORMATION: Xaa
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OTHER INFORMATION: Ceres Seq. ID 1823914
                                                                                                                                                                                                                               ORGANISM: Arabidopsis thaliana
                                                                                                        OTHER INFORMATION: Ceres Seq. ID 1823913
                                                                                                                          NAME/KEY: misc_feature
LOCATION: 1..1535
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                                                                                                                                                                                                                  FEATURE:
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LOCATION: 1..1480
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                    Local
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les 10; Conserv
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29.7%;
                  22.1%;
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Score 52; DB 5;
Pred. No. 1.5e+02;
7; Mismatches 9
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Pred. No. 1.4e+02;
7; Mismatches 9
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Pred. No.
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                                Length 1535;
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Indels
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CURRENT APPLICATION NUMBER: US/09/154,707A
CURRENT FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/05311
PRIOR PILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: US 60/041,277
PRIOR APPLICATION NUMBER: US 60/042,344
PRIOR APPLICATION NUMBER: US 60/042,344
PRIOR APPLICATION NUMBER: US 60/042,344
PRIOR APPLICATION NUMBER: US 60/041,276
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 11854
LENGTH: 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT: N. ALEXANDROV et
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Best Local
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TITLE OF INVENTION: 87
TILE REFERENCE: PZ004P1
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OTHER INFORMATION: Ceres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 KVFDKMPEKDLVAWNSVINGFAENGK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 KVFDKMPEKDLVAWNSVINGFAENGK 189
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Local Similarity 38.5%;
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                                     APPLICATION NUMBER: US 60/050,937 FILING DATE: 1997-05-30 APPLICATION NUMBER: US 60/048,187
                                                                                                              FILING DATE: 1997-05-30
                                                                                                                                   APPLICATION NUMBER: US
                                                                                                                                                                                                       FILING DATE: 1997-05-30
                                                                                                                                                                                                                            FILING DATE: 1997-05-30 APPLICATION NUMBER: US 60/048,350
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/048,094
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/041,281 FILING DATE: 1997-03-21
                                                                                                                                                                                APPLICATION NUMBER: US 60/048,188
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NUMBER: US 60/048,099
                                                                                                                                                           1997-05-30
                     1997-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 Human Secreted Proteins
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                                                                                                                                   60/048,135
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Pred. No. 1.5e+02;
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APPLICATION NUMBER: US 60/048,186

1997-05-30

1997-05-30

FILING DATE: 1997-05-30 APPLICATION NUMBER: US 60/048,352

FILING DATE:

FILING DATE:

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US-09-966-262-319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : OTHER INFORMATION: Xaa equals any of the L-amino acids commonly found US-09-154-707A-319
                                                                                                                                                                                                                                                                         Sequence 319, Application US/09966262
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC_FEATURE
LOCATION: (2)
OTHER INFORMATION: Xaa e
NAME/KEY: MISC_FEATURE
LOCATION: (114)
                                                                               PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/966,262
CURRENT FILING DATE: 2001-10-01
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PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
                                                           PRIOR
                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/0531
PRIOR FILING DATE: 1998-03-19
                                                                                                                                                                                                                                                      FILE REFERENCE: PZ004P1
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 34.1 hes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   9 PVEAAAGAGADGREPASERASRAEPPAVAMGQNDLMGTAED 49
          5 PIDAAIGGSADRNAEAFDKMKKDDQIAAAM----VLRGMAKD 42
                                                                             APPLICATION NUMBER: US 60/041,277 FILING DATE: 1997-03-21 APPLICATION NUMBER: US 60/042,344
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

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RESULT 1 US-08-252-966B-12 ; Sequence 12, Ap ; Patent No. 5634 ; GENERAL INFORM ; GENERAL INFORM ; APPLICANT: ; APPLICANT:		45	- 4-	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	
ULT 1 08-252-9668-12 equence 12, Applicat atent No. 5624818 GEMERAL INFORMATION: Elsent APPLICANT: Hurlin		44	4.4	44	44.5	44.5	44.5	45	45	45	45	45	45	45	45	45	45	45.5	
58-12 Application 5624818 FORMATION: TELSENMAN, PE		18.7	18.7		18.9		18.9	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.4	
plication US/082 818 ATION: Eisenman, Robert			35	35	861		32							506		506	338	3782	
SULT 1 -08-252-966B-12 Sequence 12, Application US/08252966B Sequence 10, 5624818 GENERAL INFORMATION: APPLICANT: Eisenman, Robert N. APPLICANT: Hurlin, Peter J.	ALIGNMENTS	1 US-08-339-152A-29	4 US-09-082-279B-940	4 US-09-082-279B-939	4 US-08-960-048-12	2 US-08-671-947-2	US-08-484-322-	S	-08-867-970-		3 US-09-108-262-2	US-08-918-509-	1 US-08-636-036-2	1 US-08-780-833-2	1 US-08-475-682-2	1 US-08-369-780-2	1 US-08-210-394-1	4 US-09-105-537-4	
		Sequence 29, Appli	940,		12,	2, 1	50,	'n	2	Ņ	2,	2,	Ņ	2	2	Sequence 2, Appli		Sequence 4, Appli	

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; ORGANISM:
US-08-252-966B-12
                                                                                                                                                                                                 TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 12:
                                                MOLECULE TYPE: proudesCRIPTION: tran
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/
FILING DATE: 01-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,99
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ITC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: FH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
                                   HYPOTHETICAL: Y ORIGINAL SOURCE:
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ayer, Donald E.
TITLE OF INVENTION: Regulatory Proteins that Dimerize with
TITLE OF INVENTION: Mad or Max
NUMBER OF SEQUENCES: 19
                                                                                                     STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1420 H
CITY: Seattle
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                  Mus musculus
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                                                                                        protein
                                                                       translation
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Query Match Best Local Similarity

21.5%; 26.7%;

Score Pred.

No. 58;

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Length 1253;

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US-08-793-229-36
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Sequence 36, Application US/08793229
Patent No. 5891703
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VAN DER LAAN, Jan Metske
APPLICANT: RIMMENS, Adriana Maxina
APPLICANT: QUAX, Wilhelmus Johannes
TITLE OF INVENTION: Mutated Penicillin
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 12; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 01-JUN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 224-07: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
DESCRIPTION: translat
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1261 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: FH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Eisenman, Robert APPLICANT: Hurlin, Peter J. APPLICANT: Ayer, Donald E.
                                                                                                                                                                                     672 LDNTLGGTSEVIHRKALQRIYADKAADIIDGLRKNPSIAVPIVLK 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Regulatory TITLE OF INVENTION: Mad or Max
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CITY: Seattle
STATE: Washing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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5624818
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                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         translation of msina9 cDNA; see Figure 29A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224-0779
                                                                                                                                                                                                                      -----ADRNAEAFDKMKKDDQIAAAMVLR 37
                                                                                                                                                                                                                                                                       21.5%; Score 50.5;
26.7%; Pred No 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Regulatory Proteins that Dimerize with
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                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36, Application US/09285957 Patent No. 6033823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 13; Conserv
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                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/285,957
                                                                                                                                                                                                                                                                                                APPLICANT: RIEMENS, Adriana Marina APPLICANT: QUAX, Wilhelmus Johannes TITLE OF INVENTION: Mutated Penicillin C Acylase Genes NUMBER OF SEQUENCES: 36
                CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (312)913-0001
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 AFLWGSADRVKEIDNRIEAYDKLTADDMWA 284
                                                   FILING DATE:
                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                        CITY: Chicago
                                                                                                                                                                                                                                                          ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff STREET: 300 South Wacker Drive
APPLICATION NUMBER:
                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 23-API
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CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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300 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                             VAN DER LAAN, Jan Metske
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-1997
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 08/793,229
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Pred. No. 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 553;
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ATTORNEY/AGENT INFORMATION:

KET NUMBER:

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US-07-941-523-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/07941523 Patent No. 5571718
                                            Matches
                                                         Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                     TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                   TOPOLOGY: 1i
MOLECULE TYPE:
17-941-523-24
                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,523
FILING DATE: 19920908
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                               NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE,DOCKET NUMBER: BN
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICALION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 AFLWGSADRVKEIDNRIEAYDKLTADDMWA 284
                                                                                                                                                                           TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Lexington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                                                         CENGTH:
 DAAIGGSADRNAEAFDKMK------
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                                                                                                                                                                                        344 amino acids
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Two Militia Drive
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WENTION: Cloning and Expression of Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
linear
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(312)913-0002
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                                             Conservative
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                                                                                                                                                linear
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                                                         Score 48.5;
Pred. No. 22;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith & Reynolds, P.C
                                             Mismatches
-----KDDQIAAAMVLRGMAKDGQFA 46
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34;
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                                            20;
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                                                                       Length 344;
                                            Indels
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US-09-117-257-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 56, Application US/08282197C Patent No. 5871730
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/117,257
CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: DET/US96/17081
EARLIER FILING DATE: 1996-10-22
EARLIER APPLICATION NUMBER: 08/589,711
EARLIER FILING DATE: 1996-01-22
EARLIER FILING DATE: 1996-01-22
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APPLICANT: Hanson, Mark
TITLE OF INVENTION: DbpA AND DbpB COMPOSITIONS AND METHODS OF
FILE REFERENCE: 4210.000500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 08/427,023 EARLIER FILING DATE: 1995-04-24
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APPLICANT: Beaulieu,
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 DAQLAAAADGNTSAISFAKGGSDAHLAGANTPKAAAVAGGIALRSLVKTGKLA 281
                                    REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 29-JUL-1994
                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                              CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                  STREET:
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1100 New York Ave.,
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                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beaulieu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brzezinski, Ryszard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                      33,851
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                                      1050.0410000
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INFORMATION FOR SEQ ID NO:

56:

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Query Match
Best Local Similarity
Thehes 13; Conserv
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; ORIGINAL SOURCE:
; ORGANISM: LCK
US-08-942-423-3
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Best Local Similarity 37.0%;
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                                                                                                                                                                                                                                                                          TELEFAX: (415) 496-3529
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                   MOLECULE TYPE: I
HYPOTHETICAL: NO
ANTI-SENSE: NO
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APPLICATION NUMBER: US 08/362,715
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: STUDIO Alto CITY: Palo Alto CITY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hashimoto, Yasuhiro
APPLICANT: Takemoto, Yoshihiro
TITLE OF INVENTION: Lck Binding Protein
NUMBER OF SEQUENCES: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/942,423 FILING DATE: 01-CCT-1997
                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 852-1698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                NAME: Peries, Rohan
REGISTRATION NUMBER: 35,752
                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 94303
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                                                                                                                                                                                                                   TOPOLOGY:
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STRANDEDNESS: bot
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3 TNPIDAAIGGSADRNAE----AFDKMKKDDQIAAAMVLR 37
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                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                            486 amino acids
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                               Conservative
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linear
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                                                                                                                          LCK BINDING PROTEIN
                                                                                                                                                                                   : protein
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                                            20.0%;
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                                                            Score 47;
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Pred. No. 44;
                                               Pred.
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                                                          Length 486;
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RESULT 10
US-09-063-035-2
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Patent No.
                                                                                                                         Query Match
Best Local Similarity
Matches 13; Conserv
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 524 amino acids
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TELEPHONE: 213/977-1001
TELEFAX: 213/977-1003
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Wong, Wean K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                             200 DPIPAPVGDSHVDSGAKSSDKQKKKTKMTDEEI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 TTPIEAASSGARGLKAKFESMAEEKRKREEEEKAQQVAR 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: NONE CLASSIFICATION: 424
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CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Wong, Wean K.
REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                                                          4 NPIDAAIGGS-ADRNAEAFDKMKK-----DDQI 30
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5. 5863532
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201 N. Figueroa St., Suite 500
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WILLIAM E. MEEK
EDWARD J. CARROLL, JR.
CURTIS A. MONNIG
                                                                                                                          Conservative
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POLYGENA T. TUAZON
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                                                                                                                                                                                                                                                               unknown
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                                                                                                                                                                                                                                                                               single
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                                                                                                                                                                                                                                                                                                                                                                                                                       33,561
                                                                                                                                                                                                                                                                                                                                             2:
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                                                                                                                                       Score 47;
Pred. No.
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                                                                                                                         Mismatches
                                                                                                                                         64;
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                                                                                                                                                   Length 524;
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                                                                                                                         Gaps
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Sequence 2, Application US/09063035 Patent No. 6160091

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GENERAL INFORMATION:

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US-08-726-012B-2
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Best Local Similarity
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                             ATTORNEY/AGENT INFORMATION:
NAME: Richard J. Polley
REGISTRATION NUMBER: 28,107
REFERENCE/DOCKET NUMBER: 381:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE: 10/04/96
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.5 inch, 1.2 Mb storage COMPUTER: IBM AT-compatible, 80486 processor OPERATING SYSTEM: MS-DOS version 6.1 SOFTWARE: WordPerfect version 8.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Disk, 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: CDNA FOR FANCONI ANEMIA COMPLEMENTATION GROUP NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 PATSP-----GGNAEALATEGGDKRAKEEKVATSTLSR 149
                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1+, ASCII
                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 97204-2988
                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         STREET: One Word CITY: Portland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 21-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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(503)
OR SEQ
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                                                                                28,107
                                                                   3812-45520/RJP/DJE
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Pred. No.
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Best Local Similarity
Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1455
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/603,803 FILING DATE: 25-OCT-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/201,762
                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                416 AQAFESCQLDSMVTAFLVVRQAALEGPSA 444
                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/660,412 FILING DATE: 22-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 19920:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: Li
                                                                                                             TOPOLOGY:
                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                NAME: Granahan, Patricia REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0' FILING DATE: 02-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
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                                                                                                                               AMINO ACID
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                                                                                                                                                .618 amino acids
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Neuroepithelial Tumors
               20.0%;
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Pred. No. 2.3e+02
             Score 47; DB 1;
Pred. No. 2.6e+02;
                             Length 1618;
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                                       US-07-925-695-9
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US-07-925-695-8
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US-07-925-695-8
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Sequence 9, Application US/07925695 Patent No. 5428145
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Best Local Similarity
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                                                                                                          1179 HAVGLFRAAVCARGVAKSIDF 1199
                                                                                                                                                                              1119 PGTKSLDPCTCGAVDLYLVTRNADVIPVRRKDDRRGALLSPRPLSTLKGSSGGPVLCSRG 1178
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NFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOPTWARE: PatentIn Release #1.0, 1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/925,695 FILING DATE: 19920807 CLASSIFICATION: 435 PRIOR APPLICATION UMBER: 10 287402/01 APPLICATION UMBER: 10 287402/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIAM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 360
APPLICATION NUMBER: JP 360
FILING DATE: 05-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Weilacher, Robert G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 287402/91 FILING DATE: 09-AUG-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
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CITY: Washington
STATE: D.C.
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TYPE: AMINO ACID
STRANDEDNESS: unl
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                                                                                                                                                                                                                   1 PLTNPIDAAIGGSAD----RNAEAFDKMKKDDQ----
                                                                                                                                                ----IAAAMVLRGMAKDGQF 45
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1850 M Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
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                                                                                                                                                                                                                                                                                                                                                                                    unknown
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DETECTION SYSTEMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetsuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP 360441/91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20,531
                                                                                                                                                                                                                                                   Score 47; DB 1; Len
Pred. No. 5.8e+02;
""matches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06/87-48009
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                                                                                                                                                                                                                                                                                         Length 3033;
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US-08-728-470-9
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                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                               Sequence 9, Application Patent No. 5928651
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 659-1462
TELEX: WUI 64470
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OKAMOTO, HI
APPLICANT: NAKAMURA, T
TITLE OF INVENTION: PC
TITLE OF INVENTION: PC
TITLE OF INVENTION: DE
NUMBER OF SEQUENCES: $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 287
FILING DATE: 09-AUG-1991
FRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 360
FILING DATE: 05-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                 TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: of NO. 5928651-Typeable Haemophilus NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESS: Shoemaker and Mattare, Ltd.
                                                                                                                                                                                                                                                                                                                                   1179 HAVGLFRAAVCARGVAKSIDF 1199
                                                                                                                                                                                                                                                                                                                                                                                                                     1119 PGTKSLDPCTCGAVDLYLVTRNADVIPVRRKDDRRGALLSPRPLSTLKGSSGGPVLCSRG 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 3033 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 20,531
REFERENCE/DOCKET NUMBER: 06/87-48009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/925,695
FILING DATE: 1920807
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                   STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza STREET: Bldg. 1
                                                                                                                                                                                                                                                                                                                                                                          30 ----IAAAMVLRGMAKDGQF 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 20.0%;
Local Similarity 22.2%;
hes 18; Conservative
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STRANDEDNESS: unl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PLTNPIDAAIGGSAD-----RNAEAFDKMKKDDQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weilacher, Robert G
                                                                                                                                                                                                                              Application US/08728470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Beveridge, DeGrandi, Weilacher & Young
1850 M Street, N.W., Suite 800
                                                                                                                                                                Barenkamp, Stephen J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Pred. No. 5.8e+02;
Pred. No. 5.8e+02;
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COMPUTER: Virginia
CONTRY: U.S.A.
ZIF: 2202-0266
ZIF: 2202-0266
ZIF: 2202-0266
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

COMPUTER:

COMPUTER:

LEBUTING DATE:

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xch completed: January 10, 2002, 14:03:58
time: 92 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: /SIDS8/gcqdata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             January 10, 2002, 14:05:14; Search time 40.15 Seconds (without alignments) 86.711 Million cell updates/sec
                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-445-803-14
235
SIDSB/gcgdata/geneseq/yeneseqp/AA1981.DAT:

SIDSB/gcgdata/geneseq/yeneseqp/AA1982.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:

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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

10 11	9	æ ~	10	տ	4	ω	2	1	Result
117 55	117	131.5	142	142	144.5	176.5	176.5	235	Score
49.8 23.4	49.8	55.3	60.4	60.4	61.5	75.1	75.1	100.0	% Query Match
26 593	26	356 256	533	156	1328	349	349	47	% Query Match Length DB
21 22	21	18	20	20	20	21	20	20	DB
AAB36280 AAG91309	AAB36273	AAW22676	AAY20112	AAY20113	AAY20088	AAB36281	AAW95612	AAW95613	SUMMARIES
B. burgdorferi var C glutamicum prote	B. burgdorferi var	B. burgdorteri ant Borrelia variable	B. burgdorferi ant	B. burgdorferi ant	B. burgdorferi ant	B. garinii P7-1 pr	Borrelia burgdorfe	Borrelia burgdorfe	2S Description

Arabidopsis thal	AAG13280	21	393	21.1	49.5	45
Arabidopsis	28	21	375	21.1		44
' Arabidopsis	AAG13282	21	344	21.1		43
Arabidopsis	AAG04817	21	327	21.1		42
Arabidopsis	AAB15081	21	324	21.1	49.5	41
S. epidermidis ope	AAG82375	22	319	21.1		40
Arabidopsis	AAG04818	21	317	21.1		39
Arabidopsis	AAG04819	21	311	21.1		38
S. epidermidis	AAG81826	22	297	21.1	•	37
S. epidermidis	AAG81486	22	297	21.1		36
Arabidopsis	AAG22847	21	287	21.1		3 5
Arabidopsis	AAG22848	21	257	21.1		34
Arabidopsis	AAG17253	21	257	21.1		33
Arabidopsis	AAG45825	21	206	21.1		32
Arabidopsis	AAG45796	21	206	21.1		31
Arabidopsis	AAG22849	21	206	21.1		30
Arabidopsis	AAG17254	21	206	21.1		29
Arabidopsis	AAG33766	21	193	21.1		28
Arabidopsis	AAG45826	21	185	21.1		27
Arabidopsis	AAG45797	21	185	21.1		26
Arabidopsis	AAG17255	21	185	21.1	•	25
Arabidopsis	AAG33767	21	183	21.1		24
Arabidopsis	AAG33768	21	177	•		23
Arabidopsis	AAG45827	21	143	•		22
Arabidopsis	AAG45798	21	143			21
Mad binding	AAW10040	18	1261	•		20
Mad binding	AAW10038	18	1253			19
Human prote:	AAB94315	22	1026	•		18
Haemophilus	AAB01826	21	975	•	•	17
Haemophilus	AAB01827	21	969		0	16
Brucella abortus	AAW48336	19	383	٠	51	15
HTRM clone 176018	AAY73333	21	127	21.7	51	14
PHA acetoacetyl-C	AAY21894	20	245		51.5	13
C glutamicum pro	AAG91164	22	354	•	2.	12

ALIGNMENTS

08-JUN-1999 (first entry)

AAW95613;

AAW95613 standard; Protein; 47

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Borrelia burgdorferi surface antigen P39.5 clone 14-1 polypeptide

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RESULT 1
AAW95613
XX AAW9561
XX O8-JUN-
XX DE BOITEL1
XX Uyme di
KW Vaccine
KW vaccine
KW antibod
XX BOITEL1
XX WO99004
XX WO99004
XX PN WO99004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lyme disease; surface antigen; P39.5; diagnosis; prevention; vaccine; antisense; therapy; treatment; primer; probe; antibody; DNA.
    WPI; 1999-095676/08
                                                                                                                                                                                                                                                                                                                                                                                                      07-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi.
                                                                              Philipp MT;
                                                                                                                                                         (TULA ) TULANE EDUCATIONAL FUND
                                                                                                                                                                                                                                            30-JUN-1997;
                                                                                                                                                                                                                                                                                                                                29-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9900413-A1
                                                                                                                                                                                                                                            97US-0051271
                                                                                                                                                                                                                                                                                                                           98WO-US13551
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/product= "clone 14-1 encoded protein"
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RESULT
AAW95612
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The sequence is that of a Borrelia burgdorferi surface antigen p39. clone 7-1 polypeptide. It can be used in the production of p39.5 or fragments of it which may be used to raise antibodies to, and in the development of vaccines against lyme disease. The sequence can also be used for making primers and probes for diagnosis, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that of a Borrelia burgdorferi surface antigen p39.5 calone 14-1 polypeptide. It can be used in the production of p39.5 or fragments of it which may be used to raise antibodies to, and in the development of vaccines against Lyme disease. The sequence can also be used for making primers and probes for diagnosis, also in DNA vaccines, as antisense therapeutics and for drug screening. Antibodiescan be used as diagnostic (immunoassay) reagents, for treating Lyme disease, for affinity purification, for drug screening and to produce anti-idiotype antibodies (used in the same way as p39.5 to induce an immune response).
                                                                                                             New nucleic acid encoding the P39.5 antigen of Borrelia burgdorferi - and related vectors, transformants, antibodies and polypeptides, for diagnosis, prevention and treatment of Lyme disease
                                                                                     Claim 5; Pages 54-55; 89pp; English.
                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                Philipp
                                                                                                                                                                                                                                           (TULA ) TULANE
                                                                                                                                                                                                                                                                        30-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                              antibody; DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyme disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi surface antigen P39.5 clone 7-1 polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW95612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW95612 standard; Protein; 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding the P39.5 antigen of Borrelia burgdorferi and related vectors, transformants, antibodies and polypeptides, for diagnosis, prevention and treatment of Lyme disease
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                                                                                                                                                                                                                                                                                                                                                                                                                           surface antigen;
sense; therapy; t
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                                                                                                                                                                                                                                           EDUCATIONAL FUND
                                                                                                                                                                                                                                                                        97US-0051271
                                                                                                                                                                                                                                                                                                  98WO-US13551
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                                                                                                                                                                                                                                                                                                                                                                                                                          treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 235; DB 20;
Pred. No. 2.4e-26;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    P39.5; diagnosis; prevention;
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                                                                                                                                                                                                                                                                                                                                                                                                                           primer;
                                                                                                                                                                                                                                                                                                                                                                                                                          probe;
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В QУ

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TNPIDAAIGGSADRN-AEAFDKMKKDDQIAAAMVLR3MAKDGQFAL 47

G.

Indels

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Gaps

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tnpidaaiggagdndaaaafatmkkddqiaaamvlr;makdgqfal 287

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AAB36281
ID AAB
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Query Match
Best Local S
Matches 38
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                        The present invention describes several peptides comprised of the invariable regions IRI-IR6 of the B. burgdorferl variable surface antigen (VisE) variable domain. These peptides can be used in the specific diagnosis, treatment and vaccination against B. burgdorferl, which causes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in DNA vaccines, as antisense therapeutics and for drug screening. Antibodies can be used as diagnostic (immunoassay) reagents, for treating Lyme disease, for affinity purification, for drug screening and to produce anti-idiotype antibodies (used in the same way as P39.5 to induce an immune response).
                                                                                                                                                                                                                                                                    Philipp MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB36281 standard; peptide;
                                                            Sequence
                                                                                                 Lyme
                                                                                                                                                                        Example
                                                                                                                                                                                             specific diagnosis of lyme
                                                                                                                                                                                                       Novel peptides comprising an invariable 26-amino acid long region isolated from Borrelia burgdorferi (sensu lato), useful for rapid
                                                                                                                                                                                                                                              WPI; 2000-687350/67.
                                                                                                                                                                                                                                                                                             (TULA ) TULANE EDUCATIONAL FUND
                                                                                                                                                                                                                                                                                                                     28-APR-1999;
                                                                                                                                                                                                                                                                                                                                             25-APR-2000; 2000WO-US11085
                                                                                                                                                                                                                                                                                                                                                                                             WO200065064-A1
                                                                                                                                                                                                                                                                                                                                                                                                                    Borrelia garinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB36281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Variable surface antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              garinii P7-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TNPIDAAIGGSADRN-AEAFDKMKKDDQIAAAMVLRGMAKDGQFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              w
                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                            borreliosis
                                                                                              disease (also known as Lyme borreliosis) in humans, dogs, horses,
 38; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
38; Conserv
                                                                                                                                                                     2; Fig
                                                                                    other
                                                            349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                   Liang FT;
                                                            AA,
                                                                                                                                                                      2; 76pp;
                                                                                    animals
                                                                                                                                                                                                                                                                                                                     99US-0300971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.1%;
82.6%;
           75.1%;
82.6%;
                                                                                                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                                      invariable region; VlsE; Lyme disease;
                                                                                                                                                                                              disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349
Score 176.5; DB 2
Pred. No. 5.5e-17;
2; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 176.5; DB 1
Pred. No. 5.5e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 20;
                      21; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                        349;
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ARZSULT
AAY2011
ID AAY2
XX
AC AAY2
XX
DT 19-J
TX
XX
BE B. b.
XX
KW Anti
XX
PN W098
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                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                         Matches
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00-JUN-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                        ery Match
                                                                                                                                                                                                                                                                                                                                          This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Borrelia burgdorferi nucleic acids products for the diagnosis, prevention and treat caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B. burgdorferi antigenic protein,
 WO9859071-A1
                      Borrelia burgdorferi
                                               Antigenic protein; vaccine;
                                                                                               19-JUL-1999
                                                                                                                       AAY20113;
                                                                                                                                             AAY20113 standard; Protein; 156 AA
                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 192-193; 275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigenic protein; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUL-1999
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                                                                                                                                                                                                           479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                       burgdorferi antigenic protein, t49-2.aa
                                                                                                                                                                                                       4 NPIDAAIG-GSADRNAEAFDKMKKDDQIAAAMVLRGMAKDGQFAL
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| 1 || || |:| | |:| | ||||||:||:||:
| 79 npiaaaigkgnaddgadfgdgmkkddqiaaaialrgmakdgkfav
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DB; AAX61785.
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32; Conservative
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                                                                                                                                                                                                                                                                                                                      1328
                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0057483.
97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                                                                                                                   61.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyme disease; infection; detection.
                                               Lyme disease; infection;
                                                                                                                                                                                                                                                       Score 144.5; DB 20;
Pred. No. 9.8e-12;
5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
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treatment of
                                                                                                                                                                                                                                                                                DB 20;
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                                               detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases
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                                                                                                                                                                                                                                                                                 1328;
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                                                                                                                                                                                                                                                         Gaps
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AAY20112
ID AAY20112
XX
XX
AC AAY2
XX
DT 19-J
XX
XX
BO B. b
XX
BO BO II
XX
WO98
XX
WO98
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WO98
XX
BO 30-[
PN 03-5
PR 20-1
PR 20-1
PR 22-1
PR 
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Best Local S
Matches 30
                                                                                                                          03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
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  Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 caused
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                                                   (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY20112 standard; Protein; 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 202; 275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated Borrelia burgdorferi nucleic acids - used products for the diagnosis, prevention and treatment of caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-189980/16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigenic protein; vaccine; Lyme disease; infection; detection.
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                                                                                                                                                                                                                                                      18-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        burgdorferi antigenic protein,
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                                                   HUMAN GENOME
MEDIMMUNE IN
                                                                                                                                                                                                                                                                                                                                                                                                        burgdorferi
  Erwin AL,
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                                                                                                                            97US-0050359.
97US-0053344.
97US-0053377.
                                                                                                                                                                                                     97US-0057483
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97US-0053344.
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  Hanson MS,
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Pred. No. 1.7e-12;
5; Mismatches 9;
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  Lathigra
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in
                                                               Claim 12;
                                                                                        caused
                                                                                              New isolated Borrelia burgdorferi nucleic acids - us products for the diagnosis, prevention and treatment
                                                                                                                                       N-PSDB;
                                                                                                                                                 WPI; 1999-189980/16
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28 npiaaaigkgnedgaefkdemkkddqiaaaiairgmakdgkfav
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                                                              Page
                                                                                       Borrelia,
                                                                                                                                                                         Erwin AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                             GENOME SCI INC
                                                                                                                                                                                                                                   97US-0057483.
97US-0050359.
97US-0053344.
97US-0053377.
                                                               193;
                                                                                                                                                                                                                                                                                               98WO-US12718
                                                            275pp;
                                                                                    particularly Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.4%;
68.2%;
                                                                                                                                                                          Hanson
                                                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 142; DB 20; L
Pred. No. 7.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168
                                                                                                                                                                          S.
                                                                                                                                                                                                                                                                                                                                                                                           Lyme disease; infection; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                        Lathigra
                                                                                      disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 533;
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                                                                                                diseases
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diseases
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RESULT
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Best Local :
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                                              28-kb linear plasmid, pBB28La, of B. burgdorferi B31 contains a vmp-like sequence (v18) locus consisting of 15 silent vls cassettes (see AAT85043) and the expressed vlsE gene. Portions of several of the 15 silent vls cassette sequences, located approx. 500 bp upstream of vlsE, recombine into the central vlsE cassette region
                                                                                                             major protein (VMP)-like protein VISE of Borrelia burgdorferi. sequence was deduced from an isolated visE gene (see ATR85042). elaborate genetic system has been identified that promotes extensive antigenic variation of VISE. An infectivity related
                                                                                                                                                                                                                    Nucleic acid encoding variable major protein-like Borrelia - useful for recombinant production of v peptide, or for diagnosis of Lyme disease
            Recombinant
                     during infection, resulting in antigenic variation and hence immune evasion, long-term survival and pathogenesis in the mammalian host.
                                                                                                                                                                                             Claim 2;
                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                           Barbour AG,
                                                                                                                                                                                                                                                                                                                                                                               21-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Variable major protein-like sequence; VMP-like sequence; VLSE; Lyme disease; relapsing fever; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW22676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW22676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                    This protein comprises the surface-exposed lipoprotein variable
                                                                                                                                                                                                                                                                                                                                                     (TEXA ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia
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DB; AAT85042.
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                                                                                                                                                                                            Page 97-99; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variable major protein (VMP)-like protein VlsE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    burgdorferi strain B31-5A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 AA;
          or native proteins expressed by VMP-like genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                           Hardham JM, Howell JK,
                                                                                                                                                                                                                                                                                                                                                     TEXAS SYSTEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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66.7%;
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Pred. No. 5.96
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ATC
                                                                                                                                                                                                                                                                                                                           Norris SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .9e-11;
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                                                                                                                                                                                                                                  e peptide
VMP like
                                                                                                                                                                                                                                                                                                                           Weinstock GM;
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immunotherapy,

immunoprophylaxis and

immunodiagnosis

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Best Local :
                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                          The present invention describes several peptides comprised of the invariable regions IRI-IR6 of the B. burgdorferi variable surface antigen (V1sE) variable domain. These peptides can be used in the specific diagnosis, treatment and vaccination against B. burgdorferi, which causes
                                                                                                                                                                                                                                                                                        Novel peptides comprising an invariable 26-amino acid long region isolated from Borrelia burgdorferi (sensu lato), useful for rapid specific diagnosis of lyme disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36273 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of Lyme disease, relapsing fever and related disorders in humans and animals. They can also be used in a Lyme disease vaccine.
           AAB36280 standard;
                                                                                                                                                                                                                                                                   Claim 1; Page 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200065064-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Variable surface antigen;
Lyme borreliosis.
                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                       WPI; 2000-687350/67.
                                                                                                                                                                                                                                                                                                                                                             Philipp MT,
                                                                                                                                                                                                                                                                                                                                                                                                        28-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                               25-APR-2000; 2000WO-US11085.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB36273;
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                                                                                                                                                                                                   Lyme
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                                                                                      24 MKKDDQIAAAMVLRGMAKDGQFAL 47
                                                               burgdorferi variable surface antigen variable domain region IR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 NPIDAAIGGSADRNAE-AFDKMKKDDQIAAAMVLRGMAKDGQFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                disease (also known as Lyme borreliosis) in humans, dogs, horses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 68.9
31; Conservative
                                                                                                                      Similarity
                                                                                                                                                                                       other animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356 AA;
                                                                                                                                                                 26 AA;
                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                            Liang FT;
                                                                                                                                                                                                                                                                                                                                                                                                        99US-0300971
                                                                                                                                                                                                                                                                  76pp; English.
          peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.3%;
                                                                                                                    49.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invariable region; VlsE; Lyme disease;
                                                                                                           0;
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          26
                                                                                                                    Score 117;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 130; DB 18; Pred. No. 2.4e-10;
           ΑA
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                                                                             18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                       Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                    Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-APR-2000; 2000WO-US11085.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Variable surface antigen; invariable region; VlsE; Lyme disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2001
                                                                                                                                                           20-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 38; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TULA ) TULANE EDUCATIONAL FUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glutamicum protein fragment SEQ ID NO: 5063.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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99JP-0377484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0300971.
                                                                                                                                                                                                                                                                                                                       glutamicum
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100.0%;
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Pred. No. 7.4e-10;
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Best Local Similarity
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  Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly I-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                             16-DEC-1999;
07-APR-2000;
                                                                                                                                                                                                                                                                                                                                         AAG91164 standard; Protein;
                                                                                                                      18-DEC-2000;
                                                                                                                                                                                                                                     Coryneform bacterium;
                                                                                                                                               20-JUN-2001.
                                                                                                                                                                         EP1108790-A2
                                                                                                                                                                                                 Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                        (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                        26-SEP-2001
                                                                                                                                                                                                                                                                                                                   AAG91164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17;
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03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                     glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                               13 SADRNAEAFDKMKKDDQIAAAMVLRGMAK 41
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                                                                                                                                                                                                                       acid synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           593
                                                                99JP-0377484.
2000JP-0159162.
2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
 Mizoguchi H,
Senoh A, Ik
                                                                                                                    2000EP-0127688
                                                                                                                                                                                                                                                            protein fragment SEQ ID NO: 4918
                                                                                                                                                                                                                                                                                       (first entry)
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2000JP-0280988.
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                                                                                                                                                                                                                                     amino
H, Ando:
Ikeda M,
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Ikeda M, Ozaki A;
                                                                                                                                                                                                                                  acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Mismatches
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Pred. No. 21;
 S, Hayashi M,
Ozaki A;
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             Ochiai
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            ζ,
            Yokoi
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RESULT :
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Best Local
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                                                                                                                                         26-DEC-1998;
19-JAN-1998;
19-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression puttern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, raccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the exemption.
                                    N-PSDB; AAX86965, AAX86968
                                                                                       Choi J,
                                                                                                                (GLDS )
                                                                                                                                                                                                                                                                          Alcaligenes latus
                                                                                                                                                                                                                                                                                                          Polyhydroxyalkanoate; PHA; PHA biosynthesis; PHA synthase; plastic; PHA beta ketothiolase; PHA acetoacetyl-CoA reductase; Alcaligenes L
                                                                                                                                                                                                                                                                                                                                                                                                                                AAY21894 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                             19-JAN-1999;
                                                                                                                                                                                                                                                WO9936547-A1
                                                                                                                                                                                                                                                                                                                                                   PHA acetoacetyl-CoA reductase sequence
                                                                                                                                                                                                                      22-JUL-1999
                                                                                                                                                                                                                                                                                                   biodegradable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 nnielqvvgsvqggvesieslkkddidfaavpfiqlva-geia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                 1999-444403/37
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                                                                                                                  LG CHEM
                                                                                    Choo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent Office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 AA;
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                     Ś
                                                                                                                                                                                                                                                                                                  polymer
                                                                                                                                         98KR-0058760.
98KR-0001422.
98KR-0001423.
                                                                                                                LTD.
                                                                                                                                                                                             99WO-KR00031.
                                                                           Han
Yoon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.3%;
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                                                                            Ξ. .~
                                                                                     Hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246pp + Sequence Listing; English
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Pred. No. 25;
8; Mismatches
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                                                                                       Lee
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                                                                                       SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 354;
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New polyhydroxyalkanoate biosynthesis-related production of biodegradable polymers

genes

used 'n

Claim

8; Page 45-56; 49pp; English.

XXX2222222222222XX

Sequence

245

A A

acid sequence of PHA acetoacetyl-CoA reductase.

The invention provides polyhydroxyalkanoate (PHA) biosynthesis-related genes. Specifically, these are the genes for PHA synthase (AAX86966), PHA beta-ketotholase (AAX86967) and PHA acetoacetyl-CoA reductase (AAX86968), derived from Alcaligenes latus. The genes are contained in fragment of 6436 nucleotides (AAX86965. The genes are used to produce recombinant proteins, which are used for PHA biosynthesis. PHA can then be used to produce biodegradable polymers, which can be used as an alternative to plastic. The production cost of PHA is much higher than those of other commercially available synthetic polymers. The present invention allows the recombinant production of PHA, which results in cheaper PHA production costs. The present sequence represents the amino

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RESULT JAAY73333 ID AAY73333 ID AAY73333 ID AAY73333 ID AAY7333 ID
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07-AUG-1998;
02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                     Hillman
Gerstin
protein sequences. The HTRM protein and nucleotide sequences are for preventing or treating disorders associated with decreased or activity of HTRM which include cell proliferative disorders arteriosclerosis and cirrhosis; cancers including adenocarcinon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTRM; human transcriptional.regulatory molecule; arteriosclerosis; AIDS; arteriosclerosis; cirrhosis; cancer; leukaemia; diabetes mellitus; Addison's disease; multiple sclerosis; rheumatoid arthritis; infection; trauma; myasthenia gravis; adenocarcinoma; immune disorder; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-NOV-1999
                                                                                                             AAY73325-Y73389 are human transcriptional regulator molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09957144-A2
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                                                                                                                                                                                                                                 peptides useful for diagnosis, prevention and treatment of cancer immune disorders \,\boldsymbol{\cdot}\,
                                                                                                                                                                                                                                                                                                                    2000-052941/04.
DB; AAZ52418.
                                                                                                                                                                      1; Page 95; 193pp; English
                                                                                                                                                                                                                                                                                                                                                                                                     EH,
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                                                                                                                                                                                                                                                                                                                                                                                                     Bandman O,
Patterson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0084254.
98US-0095827.
98US-0102745.
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m MR, 1
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No. 2
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Lu DAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245;
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                                                                                      are useful
                                                                                                                (HTRM)
                                expression such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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erythematosus, and myasthenia gravis; infections and trauma. Antagonists of the HTRM polypeptides are useful for treating or preventing disorders associated with increased expression or activity of HTRMs. HTRM polypeptides, their immunogenic fragments or oligopeptides are useful for screening libraries of compounds in drug screening techniques. Polynucleotides encoding HTRM are useful for blocking the transcription of mRNA and regulating gene function by modulating the activity of HTRM. Vectors expressing HTRM or agonists can also be used to prevent or
                                                                                                                                    treat disorder associated with decreased HTRM expression. Antibodies which specifically bind HTRM and polynucleotides encoding HTRM are useful for diagnosing disorders associated with the expression of HTRM, particularly in assays that detect the expression of HTRM. Nucleotide sequences encoding HTRM may be useful to generate hybridization probes useful in mapping the naturally occurring genomic sequence and to detect differences in gene sequences among normal, carrier and affected
Sequence
                                                individuals. Using diagnostic assays, cancer can be detected the appearance of clinical symptoms and thereby progression obe prevented by aggressive treatment or preventive measures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mellitus, rheumatoid arthritis, multiple sclerosis, systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia; immune disorders such as AIDS, Addison's disease, diabetes
   AA;
                                                                                 ed prior to
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RESULT 1
AAM448336
AAM448336
AC AAM4
XX AAM4
XX 39 k
XX 39 k
XX Bruc
XX Bruc
XX Bruc
XX Bruc
XX Bruc
XX WO98
AX C1NN
AAM4
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AA C1NN
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Best Local
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                                                                                                                                                                                                                                                                                                      N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                       Dubray G, Letesson J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 kDa antigen; detection; vaccination; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-1996;
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14; Conserv
                                                                                                                                                                                                                                                                                                      AAV17736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96EP-0870112.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 kDa antigen
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41.2%;
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Pred. No.
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12;
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The present sequence is a Brucella abortus 39 useful for in vitro detection of, or vaccinati

in

humans

or

cattle.

vaccination The antigen

against Brucella can also be used

kDa antigen

Claim

2;

Fig 3; in,

New isolated Brucella antigens of 39 developing products for detecting of,

and , or

vaccinating kDa -

against

15

useful for

e.g. humans or cattle 117pp; English

ρy B

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CC to detect and/or quantify the cellular immune response in an CC individual, or detect individuals who have been in contact with XX SO Sequence 383 AA;

Ouery Match 21.7%; Score 51; DB 19; Length 383; Best Local Similarity 34.1%; Pred. No. 46; Matches 15; Conservative 7; Mismatches 8; Indels 14; Gaps 2; Matches 15; Conservative 7; Mismatches 8; Indels 14; Gaps 2; Matches 15; Conservative 7; Mismatches 8; Indels 22; DB 185 alg--sdtmkqafdrmsklrtyvddnfsgrdwnlasamviegka 226

Search completed: January 10, 2002, 14:05:15

Job time: 169 sec
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein - protein search,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              il number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0 seq length: 2000000000
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235
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Gapop 10.0 ,
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

61.9 216 15 US-09-125-619-46	62.8 216 15 US-09-125-619-38 62.3 197 15 US-09-125-619-25	70.0 189 17 US-09-300-971A-10 63.2 179 15 US-09-125-619-18	349 17 US-09-300-971A-9 349 18 US-09-445-803-2	100.0 47 18 US-09-445-803-14	% Query Score Match Length DB ID Des
				5-803-14 Sequence	Description

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ALIGNMENTS	-09-300-	-09-300-971A	-09-300-971-	300-971-	-09-125-619-2	619-	-09-125-619-1	-09-125-619-	-US97-0Z952-	-09-125-619-4	-09-125-619-3	-09-125-619-1	-619	-09-125-619-2	-09-125-619-2	-09-125-619-3	619-4	-09-125-619-4	-09-125-619-4	-09-125-619-3	-09-125-619-1	-09-125-619-3	-09-125-619-2	619-3	-09-125-619-2		-09-125-619-2	-09-125-619-4	-09-125-619-	-09-125-619-4	-09-125-6	-09-125-619-3	-09-125-619-4	-09-125-619-3	-09-125-619-2	-300-
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RESULT

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US-09-445-803-14
); Sequence 14, Application US/09445803
; Sequence 14, Application US/09445803
; GENERAL INFORMATION:
; APPLICANT: Adminis. of Tulane Educational, Fund
; Philipp, Mario T.
; Philipp, Mario T.
; TITLE OF INVENTION: Surface Antigens and Proteins Useful in
Compositions for the Diagnosis and Prevention of Lyme
                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/445,803
FILING DATE: 13-Dec-1999
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
                      ATTORNEY/AGENT INFORMATION: NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
                                                                            APPLICATION NUMBER: US 60/051,271 FILING DATE: 30-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Spring House
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spring House Corporate Cntr., P.O. Box 457
                                                                                                                                                                                                                                                                        Version #1.30
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US-09-445-803-2

; Sequence 2, Application US/09445803

; GENERAL INFORMATION:
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JSEQUENCE 9, Application US/09300971A

GENERAL INFORMATION:

APPLICANT: Philipp, Mario T.

APPLICANT: Liang, Fang Ting

TITLE OF INVENTION:

FILE REFERENCE: TUL3USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-300-971A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; SEQUENCE DESCRIPTION: SEQ ID NO: 14: US-09-445-803-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 9
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/300,971A
CURRENT FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Borrelia garinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 349
                                                                                                                                                                                                                                                                                                                                                                                                                                  242 TNPIDAAIGGAGDNDAAAAFATMKKDDQIAAAMVLRGMAKDGQFAL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TNPIDAAIGGSADRN-AEAFDKMKKDDQIAAAMVLRGMAKDGQFAL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                 TITLE OF INVENTION: Surface Antigens
Compositions for
                                                                                                                                                                                                      NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            APPLICANT: Adminis. of Tulane Educational, Fund
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
                                                                                                                                 STATE: Pennsylvania
                                                                                                                                                     STREET: Spring House Corporate Cntr., P.O. Box 457 CITY: Spring House
                                                                                                                COUNTRY: USA
                                                                                                                                                                                       ADDRESSEE: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TUL2APCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 47 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.1%;
82.6%;
                                                                                                                                                                                                                                          Disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 176.5; DB 1
Pred. No. 4.1e-16;
2; Mismatches 5
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Pred. No. 1.3e-25;
); Mismatches 0;
                                                                                                                                                                                                                                                       and Proteins Useful in the Diagnosis and Prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 17; Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 47;
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                                                                                                                                                                                                                                                                                                                            Matches
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Sequence 18, Application US/09125619
GENERAL INFORMATION:
APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILLYN K.
APPLICANT: HOWELL, JERRILLYN K.
APPLICANT: WEINSTOCK, GEORGE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                ; LENGTH: 189
; TYPE: PRT
; ORGANISM: Borrelia burgdorfer1
US-09-300-971A-10
                                                                                                                                                                                    US-09-125-619-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-09-300-971A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09300971A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Philipp, Mario T.
APPLICANT: Liang, Fang Ting
TITLE OF INVENTION: Novel Peptides and Assays for the Diagnosis of Lyme Disease
FILE REFERENCE: TULJUSA
CURRENT APPLICATION NUMBER: US/09/300,971A
CURRENT FILING DATE: 1999-04-28
FILE REFERENCE:
                 APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                           Local Similarity es 38; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: TULZAPCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/445,803 FILING DATE: 13-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 215-540-92
TELEFAX: 215-540-5818
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UTSH: 234
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82.6%;
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Pred. No. 4.1e-16;
2; Mismatches 5
                                                                                                                                                                                                                                                                                                                                     7; Mismatches
                                                                                                                                                                                                                                                                                                                                                     Score 164.5; DB 1
Pred. No. 9.1e-15;
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US-09-125-619-18
; ORGANISM: Borrelia burgdorferi US-09-125-619-25
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Sequence 25, App...
GENERAL IMFORMATION:
GENERAL TOTAL
GENERAL TOT
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SEQ ID NO 38
LENGTH: 216
                                                                           SEQ ID NO 25
LENGTH: 197
TYPE: PRT
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Best Local Similarity 73.3%;
Matches 33; Conservative
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Best Local Similarity
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LENGTH: 179
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APPLICANT: JING-REW, ZHANG
APPLICANT: HANDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH: 234
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APPLICANT:
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CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ 4D NOS: 48
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CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
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APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: BARBOUR, ALAN G.
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CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                       SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9-125-619-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 NPIDAAIG-GSADRNAEAFDKMKKDDQIAAAMVLRGMAKDGQFAL 47
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                                                                                                                   197
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69.6%;
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Pred. No. 1.6e-12;
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US-09-125-619-19
; Sequence 19, Application US/09125619
; GENERAL INFORMATION:
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US-09-125-619-19
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; SEQ ID NO 46
; LENGTH: 216
                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 190
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                                                                                      Query Match
Best Local Similarity
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TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REPERENCE: UTSH 234
CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
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APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: BARBOUR, ALAN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILAN K.
                                                                                                                                                                                                                                                                                                                                           APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 48
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                                                                                                                                                                                                  TYPE: PRT
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Local Similarity
nes 32; Conserv
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                                     4 NPIDAAIG-GSADRNAEAFDKMKKDDQIAAAMVLRGMAKDGQFAL 47
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                                                                       Conservative
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69.6%;
                                                                                        61.5%;
71.1%;
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69.6%;
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                                                                     Score 144.5; DB 1
Pred. No. 6.5e-12;
5; Mismatches 7
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Pred. No. 5.5e-12;
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Pred. No. 3.5e-12;
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                                                                                                       DB 15; Length 190;
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CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27

NUMBER OF SEQ ID NOS: 48
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 26
SEQ ID NO 26
TYPE: PRT
ORGANISM: Borrelia burgdorferi
US-09-125-619-26
                                                                                                                                                                   RESULT 12
US-09-125-619-32
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GENERAL INFORMATION:
APPLICANT: Philipp, Mario T.
APPLICANT: Liang, Fang Ting
TITLE OF INVENTION: Novel Peptides and Assays for the Diagnosis of Lyme Disease
FILE REFERENCE: TUL3USA
CURRENT APPLICATION NUMBER: US/09/300,971A
CURRENT FILING DATE: 199-04-28
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
                                                          Sequence 32, Application US/09125619
APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26, Application US/09125619 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: WAP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN
         APPLICANT:
TITLE OF I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 323
TYPE: PRT
ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -300-971A-11
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                                                                                                                                                                                                                                                                            4 NPIDAAIGGSADRNAEAFDKMKKDDQIAAAMVLRGMAKDGQFAL 47
         OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JING-REN, ZHANG
HARDHAM, JOHN M.
HOWELL, JERRILYN K.
BARBOUR, ALAN G.
: JING-REN, ZHANG
: HARDHAM, JOHN M.
: HOWELL, JERRILYN K.
: BARBOUR, ALAN G.
: WEINSTOCK, GEORGE M.
INVENTION: VMP-LIKE SEQUENCES OF
                                                                                                                                                                                                                                                                                                                    Conservative
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68.2%;
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71.1%;
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Pred. No. 7.6e-12;
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Pred. No. 1.3e-11;
                                                                                                                                                                                                                                                                                                                  Mismatches
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   OF PATHOGENIC BORRELIA
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CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
SOETWARE: Patentin Ver. 2.1
SEQ ID NO 44
LENGTH: 212
TYPE: PRT
ORGANISM: Borrelia burgdorfer1
US-09-125-619-44
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LENGTH: 212
TYPE: PRT
ORGANISM: Borrelia burgdorferi
US-09-125-619-32
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; Sequence 36, Application US/09125619
; GENERAL INFORMATION:
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                              CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 36
LENGTH: 215
TYPE: DET
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Best Local Similarity 71.1
Matches 32; Conservative
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Best Local
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: BARBOUR, ALAN G.
                                                                                                                                              APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH: 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: WEINSTOCK, GEONGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH: 234
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CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 199-01-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                            4 NPIDAAIG-GSADRNAEAFDKMKKDDQIAAAMVLR;MAKDGQFAL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 NPIAANIGKGDADDGADEGDGMKKDDQIAAAIALRGMAKDGKEAV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity es 32; Conserv
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JING-REN, ZHANG
HARDHAM, JOHN M.
HOWELL, JERRILYN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BARBOUR, ALAN G.
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71.1%;
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71.1%;
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Pred. No. 1e-11;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 143.5; DB Pred. No. 10-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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US-09-125-619-36

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RESULT 15
US-09-125-619-16
US-09-125-619-16
Sequence 16, Application US/09125619
GENERAL INFORMATION:
APPLICANT: HORRIS, STEVEN J.
APPLICANT: HARDHAM, JOHN M.
PPLICANT: HARDHAM, JOHN M.
PPLICANT: HARDHAM, JOHN M.
PPLICANT: HARDOLR, ALAN G.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234
CUURRENT APPLICATION NUMBER: US/09/125,619
CUURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
SOCTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 169
TYPE: PRT
ORGANISM: Borrelia burgdorferi
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Search completed: January 10, 2002, 14:08:25 Job time: 359 sec
                                                                                                                                                                   Query Match 60.4%; Score 142; DB 15; Length 169; Best Local Similarity 68.2%; Pred. No. 1.3e-11; Matches 30; Conservative 5; Mismatches 9; Indels
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Best Local Similarity 71.1
Matches 32; Conservative
                                                                                          60.6%; Score 142.5; DB 15; Length 215; 71.1%; Pred. No. 1.5e-11; rative 4; Mismatches 8; Indels 1;
                                                                                                                                                                     0;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
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                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
452.5
452.5
452.5
438.8
437.5
434.5
434.5
429
421.2
421.5
421.5
420.5
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1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mamaal:*
7: sp_mhc:*
8: sp_organel1:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebrs:
13: sp_unclass:
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Match Length DB
 January 10, 2002, 14:04:01; Search time 38 Seconds (without alignments) 1343.396 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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sp_plant:*
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sp_vertebrate:*
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sp_mhc:*
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sp_bacteria:*
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 Q9RHW3
Q9RHW3
Q9RHW6
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Q9RF40
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0068375
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Q9RF43
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        O9rhw5 borrelia
O9rhw3 borrelia
O9rhw7 borrelia
O9rhw6 borrelia
O9rfw6 borrelia
O9rf40 borrelia
O06878 borrelia
O068375 borrelia
O07055 borrelia
O068368 borrelia
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O9rf44 borrelia
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O68358 borrelia
O68358 borrelia
O07053 borrelia
O07053 borrelia
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410.5	410.5	411	411.5	412	412.5	412.5	412.5	412.5	413	413	413.5	413.5	413.5	414	415	417	417	417	417.5	417.5	418	418	418.5	419	419
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221	211	222	215	214	213	213	211	211	216	214	217	215	209	216	214	216	214	212	221	211	214	212	213	218	210
ν	N	Ν	N	Ν	N	N	N	N	ν	N	N	N	N	N	2	ν	N	N	N	N	N	N	N	N	N
Q9R349.	_	Q9RF45	068364	068357	068370	068348	068379	068367	068365	068362	007061	068356	007065	068349	068303	068355	007058	007062	Q9RF38	068366	068340	068360	068354	Q9RF39	068369
borrel	borre	borrelia	porrelia	porrelia	068349 borrelia bu	borrelia	068355 borrelia bu	porrelia		porrelia	borrelia	orrelia	068360 borrelia bu	porrelia	Q9rf39 borrelia bu	orrelia									

ALIGNMENTS

Оу	Оy	Quer Best Matc		N K K			RT B	•		RP S	OX N		OS B		DT 0		AC Q	RESULT
174 NAAGAEGTTNADAGKLEVKNAGNYGGEAGDAGKAAAAVAAYSGEQIIKAIYHAAKDG 230 	117 AAVAASAATGNAAIGDVVN-GDVAKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKL 173 	Query Match 27.2%; Score 465; DB 2; Length 192; Best Local Similarity 65.2%; Pred. No. 4.3e-15; Matches 118; Conservative 13; Mismatches 38; Indels 12; Gaps 8	NON_TER 192 192 NON_TER 192 192 SEQUENCE 192 AA; 18638 MW; F45DE1DF40A81A12 CRC64;	1	InterPro; IPRA00680; Borrelia_lipo.	Microb. Pathog. 24:155-166(1998).	"Genetic and immunological analyses of VIs (VMP-like sequences) of Borrelia burgdorferi.";	Kawabata H., Myouga F., Inagaki Y., Murai N., Watanabe H.;	STRAIN= 20101050. Directoral 627.	[1] SEQUENCE FROM N.A.	NCBI_TaxID=139;	Plasmid 20.kb borrelial plasmid.	Borrelia burgdorferi (Lyme disease spirochete).	PROTE	<pre>01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)</pre>	-2000 (TrEMBLrel. 13,	Q9RHW5 PRELIMINARY; PRT; 192 AA. Q9RHW5;	5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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RESULT
QPRHW7
ID Q9
AC Q9
DT 01
DT 01
DT 01
DT 01
DT 01
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RY VI
RY VI
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RY
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Matches 118; Conserv
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EMBL; AB011067; BAA87890.1; -...
InterPro; IPR000680; Borrelia_11po.
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Q9RHW7;
01-MAY-2000 (TrEMBLrel. 13, C:
01-MAY-2000 (TrEMBLrel. 13, Lx
01-JUN-2001 (TrEMBLrel. 17, Lx
VLSII PROTEIN (FRAGMENT).
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Plasmid 20-kb borrelial plasmid.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEDLINE-98181050;
                                                    SEQUENCE FROM N.A. STRAIN=297;
                                                                                                                                                                                         Plasmid 20-kb borrelial p. Bacteria; Spirochaetales;
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O9RHW6;
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O1-MAY-2000 (TrEMBLrel. 13,
O1-JUN-2001 (TrEMBLrel. 17,
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NON_TER
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EMBL: AB011063; BAA87886.1;
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Pfam; PF00921; Lipoprotein_2;
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Plasmid 20-kb borrelial plasmid
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EMBL; AB011064; BAA87887.1; -.
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174 NAAGAEGTTNADAGKLEV----KNAGNVGGEAGDAGKAAAAVAAVSGEQILKAIVHAA-KD
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22053 MW;
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63.9%;
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                                                                                                                                                                          Score 452.5; DB 2
Pred. No. 1.6e-14;
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Pred. No. 1.6e-14;
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(VMP-like sequences)
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Best Local
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O9RE40, O1-MAY-2000 (TrEMBLrel. 13,

O1-MAY-2000 (TrEMBLrel. 13,

O1-JUN-2001 (TrEMBLrel. 17,
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Borrella burgdorferi.";
Microb. Pathog. 24:155-166(1998).
EMBL; AB011066; BAA87889.1;
ThterPro; IPR000680; Borrelia_lipo.
ThterPro; IPR000680; Borrotein_2; 1.
                                                                                                                                                     VLSE.
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01-JUN-2001 (TremBLrel. 17
VLSF15 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98181050; PubMed-9514637;
Kawabata H., Myouga F., Inagaki Y.,
"Genetic and immunological analyses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi (Lyme disease spirochete).
Plasmid 20-kb borrelial plasmid.
Bacteria; Spirochaetales; Spirochaetaceae; Borr
  SEQUENCE FROM N.A
STRAIN=W12M;
                                                                                                    Bacteria;
                                                                                                                        Borrelia burgdorferi (Lyme disease spirochete)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATAASGGKEDMIGKVVKVNAAGAAAKGGEETSVNGIASGIKGIVTAAEKA-GEEGKLKS 61
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                                                                                                    Spirochaetales;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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                                                                                                 Spirochaetaceae;
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Pred. No. 1.6e-14;
18; Mismatches 41;
                                                                                                                                                                                                Last sequence update)
Last annotation updat
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Matches 127
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Best Local
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01-JUL-1997
01-JUN-2001
VMP-LIKE VLS
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InterPro: IPR000680; Borrelia_lipo.
Pfam; PF00921; Lipoprotein_2; 1.
NON_TER 21
NON_TER 224 224
SEQUENCE 224 AA; 21807 MW; FB09
                                                                                                                                                                                                               InterPro; IPR000680; Borrelia_lipo.
pfam; PF00921; Lipoprotein_2; 1.
SEQUENCE 356 AA; 36012 MW; 3040
                                                                                                                                                                                                                                                                              STRAIN-B31 (ATCC 35210);
MEDLINE-97262068; PubMed-9108482;
Zhang J.R., Hardham J.M., Barbour A.G., Norris S.J.;
"Antigenic variation in Lyme disease borreliae by pr
recombination of VMP-like sequence cassettes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tyer R., Hardham J.M., Wormser G.P., Schwartz "Conservation and heterogeneity of visE among of Borrelia burgdorferi.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                       Cell 89:275-285(1997).
EMBL; U76405; AAC45733.1; -
                                                                                                                                                                                                                                                                                                                                                                                       Bacteria;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=139
                                                                                                                                                                                                                                                                                                                                                                                                   Borrelia burgdorferi (Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                    VLSE.
                198
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GGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPIDAAIGGAGDNDA
                                          DAAKVADKASVKGIAKGIKEIVEAAGGSE---
                                                                                                                      GKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGAEFGKDEMKKDDQIAAAIALRGMAKDGKFAVKD---DEKGRAEGA---IKGAAESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAFA--TMKKDDQIAAAMVLRGMAKDGQFALKDAAAAHEGTVKNAVDIIKAAAEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAKVADKASVTGIAKGIKEIVEAAGGSE-----KLKAVAAAKGESNKEAGKLFGKAGANN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKAKGGDAASYNGIAKGIKGIVDAAEKADAKEGKLNA-AGAEGTTNADAGKLFVKNAGNV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDV 138
                                                                    AKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNA-AGAEGTTNADAGKLFVKNAGNV
                                                                                             GKPDSTGSVGTA-----VEGAIKEVSELLDKLVKAVKTAEGASSGTAAIGEVV-ADA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDG-GEKQGKKAADRTNPIDAAIGGAGDND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKPDSTGSVGTA-----VEGAIKEVSELLDKLVKAVKTAEGASSGTAAIGEVV-ADA
                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                       Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 04, (TrEMBLrel. 04, (TrEMBLrel. 17,
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                            25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.6%;
                                                                                                                                                                                                                                                                                                                                                                                       Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                26;
                                                                                                                                                                                                                                                                                                                                                                                                      disease spirochete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
                                                                                                                                                           Score 437.5; DB 2
Pred. No. 1.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 438;
                                                                                                                                                                                                                  304035731B2AA2BE CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FB0900B833615E7B CRC64;
                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356
                                          -KLKAVAAAKGENNKGAGKLFGKAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                          Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68;
                                                                                                                                                87;
                                                                                                                                                                         <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I., Norris S.J. human and tick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 224;
                                                                                                                                                                                                                                                                                              promiscuous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                          Length
                                                                                                                                                 Indels
                                                                                                                                                31;
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                                                                                                                                                Gaps
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                                          209
                                                                    197
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                257
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RESULT
068375
ID 06
AC 06
DT 01
DT 01
DT 01
DT VY
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Best Local S
Matches 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-B31-1500B;

Zhang J.-R., Norris S.J.;

Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

SUBMI: AF034523; AAC31352.1; -.

InterPro; IPR000880; Borrelia_lipo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last amnotation update)
 Plasmid 1p28-1.
Bacteria; Spirochaetales; NCBI_TaxID~139; [1]
                                                                                        007055;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi (Lyme disease spirochete).
Plasmid 1p28-1.
Bacteria; Spirochaetales; Spirochaetaceae; Borr
NCBI_TaxID-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLSE
                                                   Borrelia burgdorferi (Lyme disease
                                                                   VLSE
                                                                               VMP-LIKE SEQUENCE
                                                                                                                                               007055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VMP-LIKE SEQUENCE PROTEIN VSLE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               068375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00921; Lipoprotein_2;
                                                                                                                                                                                                                                                                                                                                              139
                                                                                                                                                                                                               166
                                                                                                                                                                                                                           107
                                                                                                                                                                                                                                                                                           198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210
                                                                                                                                                                                                                                                                                                                  56 GAAKAADKESVKGIAKGIKEIVEAAGGSE----KLKAVAAATGENNKKAGKLFGK----
                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
mes 115; Conserv
                                                                                                                                                                                                                                                                                                                                                                     4
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                                                                                                                                                                                                                                                                                                                                  AKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNA-AGAEGTTNADAGKLFVKNAGNV 197
                                                                                                                                                                                                             GNEDGAEFNQDGMKKDDQIAAAIALRGMAKDGKFAVKDGDEKGKAEGAIKGA
                                                                                                                                                                                                                                                                            GGEAGDAG-----KAAAAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPIDAAIGG
                                                                                                                                                                                                                                                                                                                                                                     GKPDSTGSVGTA-----VEGAIKEVSELLDKLVKAVKTAEGASSGTDAIGKVVDNDA 55
                                                                                                                                                                                                                                                                                                                                                                                            GKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLGAITG--LIGDAVS-SGLRKVGDSVKAAS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AASAATGSAATGDVVNGNGATAKGGDAKSVN 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGDSEAASKAAGAVSAVSGEQILSAIVTAA-DAAEQDGKKPEEAKNPIAAAI---GDKDG
                                                                                                                                                                                                                                                              AGDAGDAGDSEAASKAAGAVSAVSGEQILSAIVKAA-DAGDQEGKKPADATNPIAAAIGK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAFA-·TMKKDDQIAAAMVLRGMAKDGQFALKDAAAAHEGTVKNAVDIIKAAAEAA--S 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217
217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      25.4%;
ilarity 49.6%;
Conservative 2
                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                               PROTEIN VLSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217
21109 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spirochaetaceae; Borrelia
                           Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 434.5; DB 2;
Pred. No. 1.3e-13;
2; Mismatches 68;
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7B34DC72AA30D83D CRC64;
                                                    spirochete).
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                                                                                                                                              358
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                217;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                         251
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Best Local Similarity
Matches 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                  STRAIN-B31-1334.,
Shang J.-R., Norris S.J.;
Shang J.-R., Norris S.J.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ
EMBL; AF034509; AAC31338.1; -.
InterPro; IPR000680; Borrelia_lipo.
InterPro; IPR000680; Borrelia_2; 1.
                                                                                                                                                                                                                                 NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               068361 PRELIMINARY; PRT; 212 AA. 068361; 01-AUG-1998 (TrEMBLrel. 07, Created) 01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00921; Lipoprotein_2; Plasmid. SEQUENCE 358 AA; 36009 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang J.R., Hardham J.M., Barbour A.G., Norris S.J. "Antigenic variation in Lyme disease borreliae by precombination of VMP-like sequence casnettes."; Cell 89:275-285(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia burgdorferi (Lyme disease spirochete).
Plasmid 1p28-1.
                                                                                                                                                                                                                                                                                                               Pfam; PF00921; Lipoprotein_2; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Spirochaetales; NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VMP-LIKE SEQUENCE PROTEIN VSLE (FRAGMENT).
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STRAIN-B31-M1E4C;
MEDLINE-97262068; PubMed-9108482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264
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                                                   79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 GKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDV 138
  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEENGAEFGDGMKKDDQIAAAIALRGMAKDGKFAVKNDDEKGKAEGA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEAGD---AGKAAAAVAAVSGEQILKAIV---HAAKDGGEKQGKKAADRTNPIDAAIGGA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKPDSTGSVGTA-----VEGAIKEVSELLDKLVKAVKTAEGASSGTAAIGEVV-ADA 153
                                                GKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAVRKVLGAITG--LIGDAVS-SGLRKVGDSVKAAS 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDNDAAAAFATMKKDDQIAAAMVLRGMAKDGQFALK--DAAAAHEGTVKNAVDIIKAAAE 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGDSEAASKAAGAVSAVSGEQILSAIVTAAGAAASEADQEGKKPADATNPIAAAIGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKAKGGDAASYNGIAKGIKGIVDAAEKADAKEGKLNAAGAEGTTNADAGKLEVKNAGNVG 198
GKPDSTGSVGTA-----VEGAIKEVSELLDKLVKAVKTAEGASSGTAAIGEVVDND-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA--SAASAATGSAAIGDVVNGNGATAKGGDAKSVN 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKA--ADKDSVKGIAKGIKEIVEAAGGSE----KLKVAAATGESNKGAGKLF----GKVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                 212
212 AA;
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                 1
212
20488 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36009 MW;
                                                                                                                        25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.4%;
                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spirochaetaceae; Borrelia
                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                   Score 429; DB 2;
Pred. No. 2.2e-13;
4; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 433.5;
                                                                                                                                                                                                                                    A98950CCEF789BDF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                        69;
                                                                                                                                                                                                                                                                                                                                                                                                                     databases
                                                                                                                                                   Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64
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                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT Q9FF44 Q9FF44 Q9PF 01 Q9 DT 01 DT 01 DT 01 DT 01 DE VLL GN VLL GN VLL GN P1-1
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068368
ID 06
AC 06
DT 01
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Best Local S
Matches 114
                                              O9RE44
O9RE44;
O1-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               068368;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                        VLSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
Borrelia burgdorferi (Lyme Plasmid 32 kb.
                                      VLSE
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1997) to the EMBL/GenBank/DDBJ EMBL; AF034516; AAC31345.1; InterPro; IPR000880; Borrelia_lipo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Spirochaetales;
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borrelia burgdorferi (Lyme disease spirochete).
Plasmid lp28-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=B31-1395F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00921; Lipoprotein_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hang J.-R., Norris S.J.;
                                                                                                                                                                                                              111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
                                                                                                                                                              167
                                                                                                                                                                                      259
                                                                                                                                                                                                                                      199
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                                                                                                                                                                                                                                                                                    139 AKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNAAGAEGTTNADAGKLFVKNAGNVG 198
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                                                                                                                                                                                                                                                                                                              4
                                  (FRAGMENT)
                                                                                                                                                                        AAFA--TMKKDDQIAAAMVLRGMAKDGQFALKDAAAAH-EGTVKNA
                                                                                                                                                                                                          GEAGDAGKAAAAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPIDAAIGGAGDNDAA 258
                                                                                                                                                                                                                                                                                                                                    GKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDSEAASKAAGAVSAVSGEQILSAIVKAA-DAAEQDGEKPAEAKNPIAAAI-GKGDGDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEAGDAGKAAAAVAAVSGEQILKAIVHAAKDGGEKQGKKAADRTNPIDAAIGGAGDNDAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKAKGGDAASVNGTAKGIKGIVDAAEKADAKEGKLNAAGAEGTTNADAGKLEVKNAGNVG
                                                                                                                                                            AEFGQDEMKKDDQIAAAIALRGMAKDGKFAVKDGEKEKAEGAIKGA
                                                                                                                                                                                                                                                             DAAKVADKASVKGIAKGIKEIVEAAGGSE----KLKAAAAEGENNKGAGKLFGKAGAAAH 110
                                                                                                                                                                                                                                                                                                             GKPDSTGSVGTA-----VEGAIKEVSELLDKLVKAVKTAEGASSGTAAIGEVV-ADA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAFAT-MKKDDQIAAAMVLRGMAKDGQFALK--DAAAAHEGTVKNA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --AKVADKASVTGIAKGIKEIVEAAGGSE----KLKVAAATGENNKGAGKLFGKAGADAH
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212
212 AA;
                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         212
20645 MW;
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17,
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           disease spirochete)
                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                         Score 428; DB 2;
Pred. No. 2.4e-13;
                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                           C7DAE7377957B175 CRC64;
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                                                                                                                                                                                    301
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79

GKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGDV 138

Query Match
Best Local Similarity
Matches 115; Conserv

Conservative

21;

Mismatches

75;

Indels

18;

Gaps

24.9%;

Score 426; Pred. No. 3

DB 2; .2e-13;

Length 223;

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QSPF43
ID QSPF43
AC QSPF43
DT 01-MAY
DT 01-MY
DT 01-JUN
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9RF43;
Q9RF43;
01-MAY-2000
01-MAY-2000
01-JUN-2001
NON_TER
NON_TER
SEQUENCE
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NON_TER
SEQUENCE
                                                                                                                                     "Conservation and heterogeneity of vlsE among of Borrelia burgdorferi."; output of vlsE among submitted (NOV-1999) to the EMBL/GenBank/DDBJ EMBL; AF201676; AAF25652.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Conservation and heterogeneity of vlsE among of Borrelia burgdorferi."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ EMBL; AF201675; AAF25651.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              VLSE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000680; Borrelia_lipo
Pfam; PF00921; Lipoprotein_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-B294;
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NCBI_TaxID=139;
[1]
                                                                                            Pfam; PF00921; Lipoprotein_2;
                                                                                                                                                                                                                                                                                                                                                    Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                          Plasmid 32
                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi
                                                                      Plasmid.
                                                                                                                                                                                                                                    Iyer R., Hardham J.M.,
                                                                                                                                                                                                                                                          STRAIN=B294;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=139;
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"Conservation and heterogeneity of vlsE among
                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGEAGDAGKAAAAVAAVSGEQILKAIVHAAKDG-GEKQGKKAADRTNPIDAAIGGAGDND 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAAKAADKASVTGIAKGIKEIVEAAGGSE----KLKAAAAAGENNKKAGKLFGKVDAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAKAKGGDAASVNGIAKGIKGIVDAAEKADAKEGKLNAAGAEGTTNADAGKLFVKNAGNV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGKPDSTGSVGTA-----VEGAIKEVSELLDKLVKAVKTAEGAPSGTDAIGEVV-AD 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGKLDATGAEGTTNVNAGKLFVKRAADDGGDADDAGKAAAAVAASAATGNAAIGDVVNGD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGADFNHEMKKDDQIAAAIALRGMAKDGKFAVKNDDEKGKAEGAIKGAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGDSEAASKAAGAVSAVSGEQILSAIVKAAAAGAAEQDGEKPADAKNPIAAAI-GKGDAD
                                                                                                                  IPR000680; Borrelia_lipo
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223 /
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0 (TrEMBLrel.
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222 /
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21635 MW;
  21636 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                  (Lyme
                                                                                                                                                                                                                                    Wormser G.P.,
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13,
17,
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                                                                                                                                                                                                                                                                                                                                                    Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                  disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 426; DB 2;
Pred. No. 3.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
  0B344689C00DC3A0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                  spirochete).
                                                                                                                                                                                                         Schwartz
/lsE among
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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                                                                                                                                                                                                            human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I., Norris S.J.
human and tick
                                                                                                                                                                databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                       Norris S.J
                                                                                                                                                                                                              tick isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
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RESULT
068358
ID 061
AC 061
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DT 01
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SEQUENCE
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ches 111; Conserv
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EMBL; U84557; AAC45194.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang J.R., Hardham J.M., Barbour A.G., Norris S.J.; "Antigenic variation in Lyme disease borreliae by promiscuous recombination of VMP-like sequence cassettes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-B31-M1E4D;
MEDLINE-97262068; PubMed-9108482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Spirochaetales;
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi (Lyme disease spirochete). Plasmid 1p28-1.
Bacteria; Spirochaetales; Spirochaetaceae; Borr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000680; Borrelia
Pfam; PF00921; Lipoprotein_2;
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|---MKKDDQIAAAIALRGMAKDGKFAVKNDEKGKAEGAIKGA 209
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(TrEMBLrel.
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20214 MW;
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49.3%; Pred. No. 3.9e-13;
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Last sequence update)
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STRAIN-B31-1380C;
STRAIN-B31-1380C;
A Zhang J.-R., Norris S.J.;
A Zhang J.-R., Norris S.J.;
A Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF034506; AAC31335.1; -.
EMBL; AF034506; Borrella_lipo.
R Ffam; PF00921; Lipoprotein_2; 1.
R Plasmid.
R PLASM
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Best Local Similarity 49.8
Matches 113; Conservative
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NCBI_TaxID-139;
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Bacteria; Spiro
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                                    AAAFA--TMKKDDQIAAAMVLRGMAKDGQFALKDAAAAH-EGTVKNA 301
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GAEFGQDEMKKDDQIAAAIALRGMAKDGKFAVKDGEKEKAEGAIKGA
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Job time: 333 sec

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1: sp_archea:*
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3: sp_fungi:*
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6: sp_mammal:*
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8: sp_organel1:
9: sp_phage:*
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Best Local Similarity
Matches 34; Conser
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MEDLINE-98181050; PubMed-9514637;
Kawabata H., Myouga F., Inagaki Y.,
"Genetic and immunological analyses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi (Lyme disease spirochete).
Plasmid 20-kb borrelial plasmid.
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
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Q9RHW7
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Microb. Pathog. 24:155-166(1998).
EMBL; AB011065; BAA87888.1; -.
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                                                                                 SEQUENCE FROM N.A.
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192 AA;
PRELIMINARY;
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18638 MW;
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72.38;
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Pred. No. 2.3e-13;
7; Mismatches 4
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 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                     Murai N., Watanabe H.; of Vls (VMP-like sequences) of
 223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 AA.
                                                                                                                                                    4; Indels
                                                                                                                                                                                  Length 192;
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110 OSPHW4

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Best Local S
Matches 34
                                                                    Query Match
Best Local Similarity 69.6
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EMBL; AB011063; BaA87886.1; -.

InterPro; IPR000680; Borreita_lipo.
Pfam; PF00921; Lipoprotein_2; 1.
Plasmid.
                                                                                                                                                                                          NON_TER
NON_TER
SEQUENCE
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SEQUENCE
                                                                                                                                                                                                                                                                                                "Genetic and immunological analyses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TremBLrel. 13,
01-MAY-2000 (TremBLrel. 13,
01-JUN-2001 (TremBLrel. 17,
VLSF15 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9RHW7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                               Pfam; PF00921; Lipoprotein_2;
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98181050; PubMed:9514637;
Kawabata H., Myouga F., Inagaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borrella burgdorferi (Lyme disease spirochete).
Plasmid 20-kb borrellal plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLSF15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9RHW4;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98181050; PubMed=9514637; Kawabata H., Wouga F., Inagaki Y., "Genetic and immunological analyses Borrelia burgdorferi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-297;
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    130
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                    NPIDAAIGGSADRNAEAF--DKMKKDDQIAAAMVLRGMAKDGQFAL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNPIDAAIGGSADRNAEAF--DKMKKDDQIAAAMVLRGMAKDGQFAL
NPTAAAIGSTGDNDAAAFSKDEMKKNDQVAAAIVLRGMAKDGEFAL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spirochaetales; Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spirochaetales; Spirochaetaceae; Borrelia
                                                                                                                                                                                    190
190
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223 AA;
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                                                                                                                                                                                            AA;
                                                                                                                                                                                        190
18748
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22053 MW;
                                                                                                    65.5%;
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72.3%;
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Last annotation update)
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Pred. No. 2.7e
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                  Score 154; DB 2; 1
Pred. No. 4.3e-12;
7; Mismatches 5;
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                                                                                                                                                                                          DF5EA566DA6D29CB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
.7e-13;
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                                                                                                                                                                                                                                                                                                                                                                                       (VMP-like
                                                                                                                                                                                                                                                                                                                                                                                                         Watanabe
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                                                                                                                          Length 190;
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                                                                                    Indels
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RESULT 068379
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Best Local S
Matches 33
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Matches
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STRAIN-B31-1502E;
Zhang J.-R., Norris S.J.;
Zhang J.-R., Norris S.J.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ
EMBL, AF034527; AAC31356.1;
InterPro: IPR000680; Borrelia_lipo.
InterPro: IPR000680; Borrelia_lipo.
                                                                                                   NON_TER
SEQUENCE
                                                                                                                               Iyer R., Hardham J.M., Wormser G.P., Schwartz "Conservation and heterogeneity of vise among of Borrelia burgdorferi.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ EMBL; AF201680; AAF25656.1;
InterPro; IPR000680; Borrelia_lipo.
Pfam; PF00921; Lipoprotein_2; 1.
                                                                                                                                                                                                                                                                                                    Q9RE39;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O68379 PRELIMINARY: PRT; 211 AA. 068379; O1-AUG-1998 (TrEMBLrel. 07, Created) O1-AUG-1998 (TrEMBLrel. 07, Last sequence update) O1-JUN-2001 (TrEMBLrel. 17, Last annotation update) WMP-LIKE SEQUENCE PROTEIN VSLE (FRAGMENT).
                                                                                                                                                                                                     STRAIN-W2F;
Iyer R., Hardham J.M.,
                                                                                                                                                                                                                                                                         Borrelia burgdorferi (Lyme disease spirochete)
                                                                                                                                                                                                                                                                                      VLSE.
                                                                                                                                                                                                                                                                                               VLSE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                       Q9RF39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Spirochaetales; Spirochaetaccae; Borrelia.
NCBI_TaxID-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi
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                                                                                                                        NON_TER
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                Bacteria;
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150 TNPIAAAIGKGNADDGADFGDGMKKDDQTAAATALRGMAKDGKFAV 195
                                                                                                                                                                                                                                                                                                                                                                                                             151 TNPIAAAIGKGDADDGAEFGNEMKKDDQIAAAIAI,RGMAKDGKFAV 196
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           TNPIDAAIG-GSADRNAEAFDKMKKDDQIAAAMVLRGMAKDGQFAL 47
                                            l Similarity
33; Conserv
                                                                                                                                                                                                                                                              Spirochaetales;
                                                                                                   218
218 AA;
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                                           63.6%;
ilarity 71.7%;
Conservative
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211
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211
20580 MW;
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21052 MW;
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71.7%;
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Last annotation updat
                                            Ų,
                                                                                                                                                                                                                                                                                                                               Created)
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                                           Score 149.5; DB 2
Pred. No. 1.9e-11;
5; Mismatches 7
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Pred. No. 1.9e-11
5; Mismatches
                                                                                                   C850839CEDA0E9E4 CRC64;
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                                                                                                                                                                                                                                                              Borrelia
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007061
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Matches 33
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Best Local
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                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                      Zhang J.R., Hardham J.M., Barbour A.G., Norris S.J.;
Zhang J.R., Hardham J.M., Barbour A.G., Norris S.J.;
"Antigenic variation in Lyme disease borreliae by promiscuous recombination of VMP-like sequence cassettes.";
Cell 89:275-285(1997).
EMBL; U84562; AAC45199.1;
InterPro; IPR000680; Borrelia_lipo.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE VLS RECOMBINATION CASSETTE VLS4 (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Spirochaetales;
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell 89:275-285(1997).
EMBL; U76406; AAC45178.1;
InterPro; IPR000680; Borrelia_lipo
                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-B31-M4B4A;
MEDLINE-97262068; PubMed-9108482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi (Lyme disease spirochete).
Plasmid 1p28-1.
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01-JUL-1997 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang J.R., Hardham J.M., Barbour A.G., Norris S.J.; "Antigenic variation in Lyme disease borreliae by promiscuous recombination of VMP-like sequence cassettes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=B31 (ATCC 35210) CLONE 5A3;
MEDLINE=97262068; PubMed=9108482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                  Plasmid.
157
                                                                                                                                                                                                                                                                                                                         Pfam; PF00921; Lipoprotein_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
NPIAAAIGKGNADDGAEFGDGMKKDDQIAAAIALRGMAKDGKFAV 201
                            NPIDAAIG-GSADRNAEAFDKMKKDDQIAAAMVLRGMAKDGQFAL 47
                                                                                                                        Similarity
                                                                                                                                                                                                                         1
217
217 AA;
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                                                                                                Conservative
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                                                                                                                                                                                                                           217
20966 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.2%;
                                                                                                                     62.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٠.
و
                                                                                              Score 147.5;
Pred. No. 3.5e
4; Mismatches
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Pred. No. 2.2e-11;
Pred. No. 2.7;
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                                                                                                                                                                                                                           619E8CA8B3A97449 CRC64;
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PRELIMINARY;

PRT; 190 AA.

006882;

01-JUL-1997 (TrEMBLrel. 04, Created)

01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

PUTATIVE VLS RECOMBINATION CASSETTE VLS5 (FRAGMENT).

Borteria; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid.
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang J.R., Hardham J.M., Barbour A.G., Norris S.J.;
"Antigenic variation in Lyme disease borreliae by proceombination of VMP-like sequence cassettes.";
Cell 89:275-285(1997).
EMBL: U84556, BAC45764.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borrelia burgdorferi (Lyme disease spirochete).
Plasmid 1p28-1.
Bacteria; Spirochaetales; Spirochaetaceae; Borr
                                                                                                                                                                                        Zhang J.R., Hardham J.M., Barbour A.G., Norris "Antigenic variation in Lyme disease borreliae, recombination of VMP-like sequence cassettes."; Cell 89:275-285(1997).
                                                                                                                                                    Pfam; PF00921; Lipoprotein_2;
                                                                                                                                                                            EMBL; U76406; AAC45179.1;
                                                                                                                                                                                                                                            MEDLINE=97262068; PubMed=9108482;
                                                                                                                                                                                                                                                      STRAIN-B31 (ATCC 35210) CLONE 5A3;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            NCBI_TaxID=139;
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                                                                                                                                                                  InterPro;
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                                                              Local Similarity
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TNPIAAATGKGNEENGAEFGDGMKKDDQIAAATALRGMAKDGKFAV 298
                         NPIDAAIG-GSADRNAEAFDKMKKDDQIAAAMVLRGMAKDGQFAL
                                                                                                                                                                IPR000680; Borrelia_lipo
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190 AA;
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nilarity 69.6%;
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18376 MW;
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71.1%;
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Pred. No. 1.1e-10;
5; Mismatches 8
                                                             Score 144.5; DB Pred. No. 7.2e-11
                                                                                                                 898EFF84308EAA7A CRC64;
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                                                  Mismatches
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Best Local Similarity 71.1
Matches 32; Conservative
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SEQUENCE
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068351;
                                                                                                                                               Zhang J.-R., Norris S.J.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ
EMBL; AF034511; AAC31340.1; -
InterPro; IPR000680; Borrelia_lipo.
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Submitted (NOV-1997) to the EMBL/Ge
EMBL; AF034498; AAC31328.1; -.
InterPro; IPR000680; Borrelia_ipo.
                                                                                                                                                                                                                                       Borrelia burgdorferi (Lyme discase spirochete).
Plasmid 1p28-1.
Bacteria; Spirochaetales; Spirochaetaceae; Borr
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VMP-LIKE SEQUENCE PROTEIN VSLE (FRAGMENT)
                                                                                                                                 Plasmid
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Plasmid lp28-1.
Bacteria; Spirochaetales; Spirochaetaceae; Borr
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212
212 AA;
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pred. No. 8.1e
5; Mismatches
                                         Score 144.5; DB 2; Pred. No. 8.2e-11; 5; Mismatches 7;
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RESULT 12
068354
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AC 068354
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DT 01-JUN
DE VMP-LI
GN VLSE.
OS BOITEL
OG BACTER
OC BACTER
COX NCBL_T
RN [1]
RP SEQUEN
RC STRAIN
RC STRAIN
RC STRAIN
RA SUBMITEL
DR EMBL;
DR Interp
DR Pfam;
KW Plasmi
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STRAIN-B31-1375A;
Zhang J.-R., NOTIS S.J.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ
SUBMITTED (NOV-1997) to the EMBL/GenBank/DDBJ
EMBL; AF034501; AAC31331.1; ...
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
VMP-LIKE SEQUENCE PROTEIN VSLE (FRAGMENT).
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                                                                                                                                                                                                                                                        Pfam; PF00921; Lipoprotein_2; Plasmid.
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MEDLINE-97262068; PubMed=9108482;
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Bacteria; Spirochaetales; Spirochaetaceae;
NCBI_TaxID~139;
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Pfam; PF00921; Lipoprotein_2; 1.
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Bacteria; Spiro
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                                                                      Local Similarity
les 32; Conserv
4 NPIDAAIG-GSADRNAEAFDKMKKDDQIAAAMVLRGMAKDGQEAL 47
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U84558; AAC45195.1; -
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213
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                                                                      Conservative
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                                                                 Score 144.5; DB 2; Pred. No. 8.2e-11; 5; Mismatches 7;
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154 NPIAAAIGKGNADDGADFGDGMKKDDQIAAAIALRGMAKDGKFAV 198

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Best Local Similarity 68.2
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Borrella burgdorferi (Lyme disease spirochete).

Plasmid 1p28-1.

Bacteria: Spirochaetales; Spirochaetaceae; Borrelia.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=B31 (ATCC 35210) CLONE 5A3;
MEDLINE=97262068; PubMed=9108482;
Zhang J.R., Hardham J.M., Barbour A.G., Norris S.J.;
Zeong J. Hardham J. Hardham J.M., Barbour A.G., Norris S.J.;
Zeong J. Hardham J.M., Barbour A.G., Norris S.J.;
Zeong J. Hardham J.
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STRAIN-B31-1413A;
STRAIN-B31-1413A;
Zhang J.-R., NORTIS S.J.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF034519; AAC31348.1;
HSSP; P448781; 1B67.
InterPro; IPR000680; Borrelia_lipo.
Pfam; PF00921; Lipoprotein_2; 1.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE VLS RECOMBINATION CASSETTE VLS12 (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VMP-LIKE SEQUENCE PROTEIN VSLE (FRAGMENT).
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136 NPIAAAIGKGNENGAEFKDEMKKDDQIAAAIALRGMAKDGKFAV 179
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215 AA;
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189 AA;
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                                                                                                                                                   Score 143.5; DB 2; Length Pred. No. 1.1e-10; 6; Mismatches 7; Indels
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Db 156 NPIAAAIGKGNEENGAEFKDEMKKDDQIAAAIALRGMAKDGKFAV 200

Search completed: January 10, 2002, 14:09:35 Job time: 334 sec